

SEQUENCE LISTING

<110> Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of
Flavivirus Infection

<130> 14114.0332U3

<150> PCT/US99/12298

<151> 1999-06-03

<150> 09/701,536

<151> 2000-11-29

<150> 60/087,908

<151> 1998-06-04

<160> 31

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (25)...(48)

<221> misc_feature

<222> 1-48

<223> Amplimer 14DV389

<400> 1

cttggtacct cttagagccgc cgcc atg ggc aga aag caa aac aaa aga
Met Gly Arg Lys Gln Asn Lys Arg

48

1

5

<210> 2

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 2

Met Gly Arg Lys Gln Asn Lys Arg

1

5

<210> 3

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-50

<223> Amplimer c14DV2453

<400> 3

ttttctttttg cggccgctca aacttaagca tgcacattgg tcgctaagaa

50

<210> 4

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (25)...(48)

<221> misc_feature

<222> (1)...(48)

<223> Amplimer YFDV389

<400> 4

cttggtagcct ctagagccgc cgcc atg cgt tcc cat gat gtt ctg act

48

Met Arg Ser His Asp Val Leu Thr

1

5

<210> 5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 5

Met Arg Ser His Asp Val Leu Thr
1 5

<210> 6

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-41

<223> Amplimer cYFDV2452

<400> 6

ttttctttttg cgcccgctca cgccccaact cctagagaaa c

41

<210> 7

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (25)...(54)

<221> misc_feature

<222> 1-54

<223> Amplimer SLEDV410

<400> 7

cttggtacct ctagagccgc cgcc atg tct aaa aaa aga gga ggg acc aga
Met Ser Lys Lys Arg Gly Gly Thr Arg
1 5

51

<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 8

Met Ser Lys Lys Arg Gly Gly Thr Arg

1

5

<210> 9

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-38

<223> Amplimer cSLEDV2449

<400> 9

ttttcttttg cggccgctta ggcttgcacg ctggttgc

38

<210> 10

<211> 7500

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (916)...(3009)

<221> misc_feature

<222> 1-7500

<223> pCDJE 2-7

<400> 10

| | | | | | | |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| gacggatcgg | gagatctccc | gatcccctat | ggtcgactct | cagtacaatc | tgctctgatg | 60 |
| ccgcatagtt | aagccagtat | ctgctccctg | cttgtgtgtt | ggaggtcgct | gagtagtgcg | 120 |
| cgagcaaaat | ttaagctaca | acaaggcaag | gcttgaccga | caattgcatg | aagaatctgc | 180 |
| ttagggttag | gcgtttttgcg | ctgcttcgcg | atgtacgggc | cagatatacg | cgttgacatt | 240 |
| gattattgac | tagttattaa | tagtaatcaa | ttacggggtc | attagttcat | agcccatata | 300 |
| tggagttccg | cgttacataa | cttacggtaa | atggcccggc | tggctgaccg | cccaacgacc | 360 |
| cccgcgccatt | gacgtcaata | atgacgtatg | ttcccatagt | aacgccaata | gggactttcc | 420 |
| attgacgtca | atgggtggac | tattttacggt | aaactgccca | cttggcagta | catcaagtgt | 480 |
| atcatatgcc | aagtaagccc | cctattgacg | tcaatgacgg | taaatggccc | gcctggcatt | 540 |
| atgcccagta | catgacctta | tgggactttc | ctacttggca | gtacatctac | gtattagtca | 600 |
| tcgctattac | catggtgatg | cggtttttggc | agtacatcaa | tgggcgtgga | tagcggtttg | 660 |
| actcacgggg | atttccaagt | ctccacccca | ttgacgtcaa | tgggagtttg | ttttggcacc | 720 |
| aaaatcaacg | ggactttcca | aaatgtcgta | acaactccgc | cccattgacg | caaaggggcg | 780 |
| gtaggcgtgt | acggtgggag | gtctatataa | gcagagctct | ctggctaact | agagaaccca | 840 |
| ctgcttactg | gcttatcgaa | attaatacga | ctcactatag | ggagacccaa | gcttgggtacc | 900 |

| | |
|--|------|
| gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa | 951 |
| Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu | |
| 1 5 10 | |
| ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg | 999 |
| Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala | |
| 15 20 25 | |
| gga gcc atg aag ttg tgc aat ttc cag ggg aag ctt ttg atg acc atc | 1047 |
| Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile | |
| 30 35 40 | |
| aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga | 1095 |
| Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly | |
| 45 50 55 60 | |
| gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag | 1143 |
| Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu | |
| 65 70 75 | |
| gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca | 1191 |
| Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro | |
| 80 85 90 | |
| gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat | 1239 |
| Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr | |
| 95 100 105 | |
| gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg | 1287 |
| Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val | |
| 110 115 120 | |
| tgc gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct | 1335 |
| Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala | |
| 125 130 135 140 | |
| tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac | 1383 |
| Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn | |
| 145 150 155 | |
| tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc | 1431 |
| Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly | |
| 160 165 170 | |
| tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc | 1479 |
| Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu | |
| 175 180 185 | |
| ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc | 1527 |
| Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly | |
| 190 195 200 | |

14114.0332U3

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| aat Asn 205 | cgt Arg | gac Asp | ttc Phe | ata Ile | gaa Glu 210 | gga Gly | gcc Ala | agt Ser | gga Gly | gcc Ala 215 | act Thr | tgg Trp | gtg Val | gac Asp | ttg Leu 220 | 1575 |
| gtg Val | ctg Leu | gaa Glu | gga Gly | gat Asp 225 | agc Ser | tgc Cys | ttg Leu | aca Thr | atc Ile 230 | atg Met | gca Ala | aac Asn | gac Asp | aaa Lys 235 | cca Pro | 1623 |
| aca Thr | ttg Leu | gac Asp | gtc Val 240 | cgc Arg | atg Met | att Ile | aac Asn | atc Ile 245 | gaa Glu | gct Ala | agc Ser | caa Gln | ctt Leu 250 | gct Ala | gag Glu | 1671 |
| gtc Val | aga Arg | agt Ser 255 | tac Tyr | tgc Cys | tat Tyr | cat His | gct Ala 260 | tca Ser | gtc Val | act Thr | gac Asp | atc Ile 265 | tcg Ser | acg Thr | gtg Val | 1719 |
| gct Ala 270 | cgg Arg | tgc Cys | ccc Pro | acg Thr | act Thr | gga Gly 275 | gaa Glu | gcc Ala | cac His | aac Asn 280 | gag Glu | aag Lys | cga Arg | gct Ala | gat Asp | 1767 |
| agt Ser 285 | agc Ser | tat Tyr | gtg Val | tgc Cys | aaa Lys 290 | caa Gln | ggc Gly | ttc Phe | act Thr | gac Asp 295 | cgt Arg | ggg Gly | tgg Trp | ggc Gly | aac Asn 300 | 1815 |
| gga Gly | tgt Cys | gga Gly | ctt Leu | ttc Phe 305 | ggg Gly | aag Lys | gga Gly | agc Ser | att Ile 310 | gac Asp | aca Thr | tgt Cys | gca Ala | aaa Lys 315 | ttc Phe | 1863 |
| tcc Ser | tgc Cys | acc Thr | agt Ser 320 | aaa Lys | gcg Ala | att Ile | ggg Gly | aga Arg | aca Thr 325 | atc Ile | cag Gln | cca Pro | gaa Glu 330 | aac Asn | atc Ile | 1911 |
| aaa Lys | tac Tyr 335 | gaa Glu | gtt Val | ggc Gly | att Ile | ttt Phe 340 | gtg Val | cat His | gga Gly | acc Thr | acc Thr 345 | act Thr | tcg Ser | gaa Glu | aac Asn | 1959 |
| cat His 350 | ggg Gly | aat Asn | tat Tyr | tca Ser | gcg Ala | caa Gln 355 | gtt Val | ggg Gly | gcg Ala | tcc Ser | cag Gln 360 | gcg Ala | gca Ala | aag Lys | ttt Phe | 2007 |
| aca Thr 365 | gta Val | aca Thr | ccc Pro | aat Asn | gct Ala 370 | cct Pro | tcg Ser | ata Ile | acc Thr | ctc Leu 375 | aaa Lys | ctt Leu | ggt Gly | gac Asp | tac Tyr 380 | 2055 |
| gga Gly | gaa Glu | gtc Val | aca Thr | ctg Leu 385 | gac Asp | tgt Cys | gag Glu | cca Pro | agg Arg 390 | agt Ser | gga Gly | ctg Leu | aac Asn | act Thr 395 | gaa Glu | 2103 |
| gcg Ala | ttt Phe | tac Tyr 400 | gtc Val | atg Met | acc Thr | gtg Val | ggg Gly | tca Ser | aag Lys 405 | tca Ser | ttt Phe | ctg Leu 410 | gtc Val | cat His | agg Arg | 2151 |
| gag | tgg | ttt | cat | gac | ctc | gct | ctc | ccc | tgg | acg | tcc | cct | tcg | agc | aca | 2199 |

| | |
|---|------|
| Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr | |
| 415 420 425 | |
| gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc | 2247 |
| Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala | |
| 430 435 440 | |
| aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat | 2295 |
| Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His | |
| 445 450 455 460 | |
| cag gcg ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag | 2343 |
| Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys | |
| 465 470 475 | |
| tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct | 2391 |
| Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala | |
| 480 485 490 | |
| ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg | 2439 |
| Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala | |
| 495 500 505 | |
| aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc | 2487 |
| Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser | |
| 510 515 520 | |
| tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg | 2535 |
| Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala | |
| 525 530 535 540 | |
| agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc | 2583 |
| Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro | |
| 545 550 555 | |
| ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa | 2631 |
| Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu | |
| 560 565 570 | |
| ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag | 2679 |
| Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln | |
| 575 580 585 | |
| atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt | 2727 |
| Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe | |
| 590 595 600 | |
| tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca | 2775 |
| Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr | |
| 605 610 615 620 | |
| gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa | 2823 |
| Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys | |
| 625 630 635 | |

2025 RELEASE UNDER E.O. 14176

| | |
|--|------|
| gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga | 2871 |
| Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly | |
| 640 645 650 | |
| atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg | 2919 |
| Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met | |
| 655 660 665 | |
| ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca | 2967 |
| Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr | |
| 670 675 680 | |
| ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct taa | 3009 |
| Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala * | |
| 685 690 695 | |
| ttagtttgag cggccgctcg agcatgcato tagagggccc tattctatag tgtcacctaa | 3069 |
| atgctagagc tcgctgatca gcctcgactg tgccttctag ttgccagcca tctgttgttt | 3129 |
| gcccccccc cgtgccttcc ttgacctgg aaggtgccac tcccactgtc ctttccta | 3189 |
| aaaatgagga aattgcatcg cattgtctga gtaggtgtca ttctattctg gggggtggg | 3249 |
| tggggcagga cagcaagggg gaggattggg aagacaatag caggcatgct ggggatgcg | 3309 |
| tgggtctat ggcttctgag gcggaaagaa ccagctgggg ctctaggggg tatccccacg | 3369 |
| cgccctgtag cggcgcatta agcgcggcgg gtgtggtggt tacgcgcagc gtgaccgcta | 3429 |
| cacttgccag cgccctagcg ccgcctcctt tcgcttctt cccctcctt ctcgccacgt | 3489 |
| tcgccggctt tccccgtcaa gctctaaatc ggggcacccc tttagggttc cgatttagtg | 3549 |
| ctttacggca cctcgacccc aaaaaacttg attagggtga tggttcacgt agtgggccat | 3609 |
| cgccctgata gacgggtttt cgccctttga cgttggagtc cagtttctt aatagtggac | 3669 |
| tcttgttcca aactggaaca acactcaacc ctatctcggt ctattctttt gatttataag | 3729 |
| ggattttggg gatttcggcc tattggttaa aaaatgagct gatttaacaa aaatttaacg | 3789 |
| cgaattaatt ctgtggaatg tgtgtcagtt aggggtgtgga aagtccccag gctccccagg | 3849 |
| caggcagaag tatgcaaagc atgcattctca attagtcagc aaccagggtg ggaaagtccc | 3909 |
| caggctcccc agcaggcaga agtatgcaaa gcatgcattt caattagtca gcaaccatag | 3969 |
| tcccgccctt aactccgccc atcccccccc taactccgcc cagttccgcc cattctccgc | 4029 |
| cccatggctg actaattttt tttatttatg cagaggccga ggccgcctct gcctctgagc | 4089 |
| tattccagaa gtagtgagga ggcttttttg gaggcctagg cttttgcaaa aagctcccg | 4149 |
| gagcttgat atccattttt ggatctgatc aagagacagg atgaggatcg tttcgcatga | 4209 |
| ttgaacaaga tggattgcac gcagggttctc cgcccgcttg ggtggagagg ctattcggct | 4269 |
| atgactgggc acaacagaca atcggtgct ctgatgccgc cgtgttccg ctgtcagcgc | 4329 |
| agggcgccc ggttctttt gtcaagaccg acctgtccg tgccctgaat gaactgcagg | 4389 |
| acgaggcagc gcggtatcg tggctggcca cgacgggctg tccttgcgca gctgtgctcg | 4449 |
| acgttgtcac tgaagcggga agggactggc tgctattggg cgaagtgccg gggcaggatc | 4509 |
| tcctgtcatc tcaccttgct cctgccgaga aagtatccat catggctgat gcaatgcggc | 4569 |
| ggctgcatac gcttgatccg gctacctgcc cattcgacca ccaagcgaaa catcgcatcg | 4629 |
| agcgagcacg tactcggatg gaagcgggtc ttgtcgatca ggatgatctg gacgaagagc | 4689 |
| atcaggggct cgcgccagcc gaactgttcg ccaggctcaa ggcgcgatg cccgacggcg | 4749 |
| aggatctcgt cgtgacccat ggcatgcct gcttgccgaa tatcatggtg gaaaatggcc | 4809 |
| gcttttctgg attcatcgac tgtggccggc tgggtgtggc ggaccgctat caggacatag | 4869 |
| cgttggctac ccgtgatatt gctgaagagc ttggcggcga atgggctgac cgcttctc | 4929 |
| tgctttacgg tatcgccgct cccgatccgc agcgcacgc cttctatcgc cttcttgacg | 4989 |
| agttcttctg agcgggactc tggggttcga aatgaccgac caagcgacgc ccaacctgcc | 5049 |
| atcacgagat ttcgattcca ccgcgcctt ctatgaaagg ttgggcttcg gaatcgttt | 5109 |
| ccgggacgcc ggctggatga tctccagcg cggggatctc atgctggagt tcttcgcca | 5169 |
| cccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca tcacaaattt | 5229 |


```

cacaaataaa gcattttttt cactgcattc tagttgtggt ttgtccaaac tcatcaatgt 5289
atcttatcat gtctgtatac cgctgacctc tagctagagc ttggcgtaat catggtcata 5349
gctgtttcct gtgtgaaatt gttatccgct cacaattcca cacaacatac gagccggaag 5409
cataaagtgt aaagcctggg gtgcctaata agtgagctaa ctcacattaa ttgcgttgcg 5469
ctcactgccg gctttccagt cgggaaacct gtcgtgccag ctgcattaat gaatcgcca 5529
acgcgcgggg agaggcggtt tgcgtattgg gcgctcttcc gcttcctcgc tctactgactc 5589
gctgcgctcg gtcgttcggc tgcggcgagc ggtatcagct cactcaaagg cggtaatacg 5649
gttatccaca gaatcagggg ataacgcagg aaagaacatg tgagcaaaag gccagcaaaa 5709
ggccaggaac cgtaaaaagg ccgcgttgct ggcgtttttc cataggctcc gccccctga 5769
cgagcatcac aaaaatcgac gctcaagtca gaggtggcga aaccgcagag gactataaag 5829
ataccaggcg tttccccctg gaagctccct cgtgcgctct cctgttcga ccctgccgct 5889
taccggatac ctgtccgctt ttctcccttc gggaagcgtg gcgctttctc aatgctcacg 5949
ctgtaggtag ctcatgttcg tgtaggctgt tcgctccaag ctgggctgtg tgcacgaacc 6009
ccccgttcag ccgcaccgct gcgccttata cggtaactat cgtcttgagt ccaaccgggt 6069
aagacacgac ttatcgccac tggcagcagc cactggtaac aggattagca gagcgaggta 6129
tgtaggcggt gctacagagt tcttgaagtg gtggcctaac tacggctaca ctagaaggac 6189
agtatttggt atctgcgctc tgctgaagcc agttaccttc ggaaaaagag ttggtagctc 6249
ttgatccggc aaacaaacca ccgctggtag cgggtggtttt tttgtttgca agcagcagat 6309
tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc ttttctacgg ggtctgacgc 6369
tcagtggaac gaaaactcac gttaagggat tttggtcatg agattatcaa aaaggatctt 6429
cacctagatc cttttaaatt aaaaatgaag ttttaaatac atctaaagta tatatgagta 6489
aacttggtct gacagttacc aatgcttaac cagtgaggca cctatctcag cgatctgtct 6549
atttcgttca tccatagttg cctgactccc cgtcgtgtag ataactacga tacgggaggg 6609
cttaccatct ggccccagtg ctgcaatgat accgcgagac ccacgctcac cggctccaga 6669
tttaccagca ataaaccagc cagccggaag ggccgagcgc agaagtggtc ctgcaacttt 6729
atccgcctcc atccagtcta ttaattgttg ccgggaagct agagtaagta gttcgccagt 6789
taatagtttg cgcaacgttg ttgocattgc tacaggcatc gtggtgtcac gctcgtcgtt 6849
tggtatggct tcattcagct ccggttccca acgatcaagg cgagttacat gatcccccat 6909
gttgtgcaaa aaagcgggta gctccttcgg tcctccgacg gttgtcagaa gtaagttggc 6969
cgcagtgtta tctactatgg ttatggcagc actgcataat tctcttactg tcatgccatc 7029
cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag tcattctgag aatagtgtat 7089
gcggcgaccg agttgctctt gcccggcgct aatacgggat aataccgcgc cacatagcag 7149
aactttaaaa gtgctcatca ttggaaaacg ttcttcgggg cgaaaactct caaggatctt 7209
accgctgttg agatccagtt cgatgtaacc cactcgtgca cccaactgat cttcagcatc 7269
ttttactttc accagcgttt ctgggtgagc aaaaacagga aggcaaaatg ccgcaaaaaa 7329
gggaataagg gcgacacgga aatggtgaat actcatactc ttcttttttc aatattattg 7389
aagcatttat caggggttatt gtctcatgag cggatacata tttgaatgta tttagaaaaa 7449
taaacaaata ggggttcgcg gcacatttcc ccgaaaagtg ccacctgacg t 7500

```

<210> 11

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCDJE 2-7

<400> 11

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Lys | Gln | Asn | Lys | Arg | Gly | Gly | Asn | Glu | Gly | Ser | Ile | Met |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Trp | Leu | Ala | Ser | Leu | Ala | Val | Val | Ile | Ala | Cys | Ala | Gly | Ala | Met | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Ser | Asn | Phe | Gln | Gly | Lys | Leu | Leu | Met | Thr | Ile | Asn | Asn | Thr | Asp |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Ile | Ala | Asp | Val | Ile | Val | Ile | Pro | Thr | Ser | Lys | Gly | Glu | Asn | Arg | Cys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Trp | Val | Arg | Ala | Ile | Asp | Val | Gly | Tyr | Met | Cys | Glu | Asp | Thr | Ile | Thr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Tyr | Glu | Cys | Pro | Lys | Leu | Thr | Met | Gly | Asn | Asp | Pro | Glu | Asp | Val | Asp |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Cys | Trp | Cys | Asp | Asn | Gln | Glu | Val | Tyr | Val | Gln | Tyr | Gly | Arg | Cys | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Arg | Thr | Arg | His | Ser | Lys | Arg | Ser | Arg | Arg | Ser | Val | Ser | Val | Gln | Thr |
| | 115 | | | | | 120 | | | | | | 125 | | | |
| His | Gly | Glu | Ser | Ser | Leu | Val | Asn | Lys | Lys | Glu | Ala | Trp | Leu | Asp | Ser |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Thr | Lys | Ala | Thr | Arg | Tyr | Leu | Met | Lys | Thr | Glu | Asn | Trp | Ile | Ile | Arg |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Asn | Pro | Gly | Tyr | Ala | Phe | Leu | Ala | Ala | Val | Leu | Gly | Trp | Met | Leu | Gly |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ser | Asn | Asn | Gly | Gln | Arg | Val | Val | Phe | Thr | Ile | Leu | Leu | Leu | Leu | Val |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ala | Pro | Ala | Tyr | Ser | Phe | Asn | Cys | Leu | Gly | Met | Gly | Asn | Arg | Asp | Phe |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ile | Glu | Gly | Ala | Ser | Gly | Ala | Thr | Trp | Val | Asp | Leu | Val | Leu | Glu | Gly |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asp | Ser | Cys | Leu | Thr | Ile | Met | Ala | Asn | Asp | Lys | Pro | Thr | Leu | Asp | Val |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Arg | Met | Ile | Asn | Ile | Glu | Ala | Ser | Gln | Leu | Ala | Glu | Val | Arg | Ser | Tyr |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Cys | Tyr | His | Ala | Ser | Val | Thr | Asp | Ile | Ser | Thr | Val | Ala | Arg | Cys | Pro |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Thr | Thr | Gly | Glu | Ala | His | Asn | Glu | Lys | Arg | Ala | Asp | Ser | Ser | Tyr | Val |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Cys | Lys | Gln | Gly | Phe | Thr | Asp | Arg | Gly | Trp | Gly | Asn | Gly | Cys | Gly | Leu |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Phe | Gly | Lys | Gly | Ser | Ile | Asp | Thr | Cys | Ala | Lys | Phe | Ser | Cys | Thr | Ser |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Lys | Ala | Ile | Gly | Arg | Thr | Ile | Gln | Pro | Glu | Asn | Ile | Lys | Tyr | Glu | Val |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Gly | Ile | Phe | Val | His | Gly | Thr | Thr | Thr | Ser | Glu | Asn | His | Gly | Asn | Tyr |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ser | Ala | Gln | Val | Gly | Ala | Ser | Gln | Ala | Ala | Lys | Phe | Thr | Val | Thr | Pro |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Asn | Ala | Pro | Ser | Ile | Thr | Leu | Lys | Leu | Gly | Asp | Tyr | Gly | Glu | Val | Thr |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Leu | Asp | Cys | Glu | Pro | Arg | Ser | Gly | Leu | Asn | Thr | Glu | Ala | Phe | Tyr | Val |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Met | Thr | Val | Gly | Ser | Lys | Ser | Phe | Leu | Val | His | Arg | Glu | Trp | Phe | His |
| | | | | 405 | | | | | 410 | | | | | 415 | |

11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500

```

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
      420                      425                      430
Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
      435                      440                      445
Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
      450                      455                      460
Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
465                      470                      475                      480
His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
      485                      490                      495
Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
      500                      505                      510
Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
      515                      520                      525
Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
      530                      535                      540
Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
545                      550                      555                      560
Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
      565                      570                      575
Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
      580                      585                      590
Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
      595                      600                      605
Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
      610                      615                      620
Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
625                      630                      635                      640
Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
      645                      650                      655
Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
      660                      665                      670
Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
      675                      680                      685
Val Phe Leu Ala Thr Asn Val His Ala
      690                      695

```

<210> 12

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-46

<223> WN 466

<400> 12

cttggtaccc gtctcggcgc cgtgaccctc tcgaacttcc agggca

<210> 13
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-43
<223> CWN2444

<400> 13
agaggcactt gcacgtgcgg acttcogccg gcgaaaaaga aaa

43

<210> 14
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<223> JE Signal

<400> 14
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15
Val Val Ile Ala Cys Ala Gly Ala
20

<210> 15
<211> 5308
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> CDS
<222> (911)...(2987)

<221> misc_feature
<222> (1)...(5308)
<223> pCBWN

<400> 15
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctgatg 60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala

10

25

45

60

75

90

105

125

140

155

| | |
|---|------|
| tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc | 1429 |
| Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr | |
| 160 165 170 | |
| atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct | 1477 |
| Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala | |
| 175 180 185 | |
| tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga | 1525 |
| Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly | |
| 190 195 200 205 | |
| gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc | 1573 |
| Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys | |
| 210 215 220 | |
| gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg | 1621 |
| Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met | |
| 225 230 235 | |
| aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg | 1669 |
| Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu | |
| 240 245 250 | |
| gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga | 1717 |
| Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly | |
| 255 260 265 | |
| gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa | 1765 |
| Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln | |
| 270 275 280 285 | |
| gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa | 1813 |
| Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys | |
| 290 295 300 | |
| gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata | 1861 |
| Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile | |
| 305 310 315 | |
| gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt | 1909 |
| Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe | |
| 320 325 330 | |
| gtc cat gga cca act act gtg gag tcg cac gga aac tac tcc aca cag | 1957 |
| Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln | |
| 335 340 345 | |
| gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct | 2005 |
| Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro | |
| 350 355 360 365 | |
| tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt | 2053 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Ser | Tyr | Thr | Leu | Lys | Leu | Gly | Glu | Tyr | Gly | Glu | Val | Thr | Val | Asp | Cys | |
| | | | | 370 | | | | | 375 | | | | | 380 | | |
| gaa | cca | cgg | tca | ggg | att | gac | acc | aat | gca | tac | tac | gtg | atg | act | gtt | 2101 |
| Glu | Pro | Arg | Ser | Gly | Ile | Asp | Thr | Asn | Ala | Tyr | Tyr | Val | Met | Thr | Val | |
| | | | | 385 | | | | | 390 | | | | | 395 | | |
| gga | aca | aag | acg | ttc | ttg | gtc | cat | cgt | gag | tgg | ttc | atg | gac | ctc | aac | 2149 |
| Gly | Thr | Lys | Thr | Phe | Leu | Val | His | Arg | Glu | Trp | Phe | Met | Asp | Leu | Asn | |
| | | | | 400 | | | | | 405 | | | | | 410 | | |
| ctc | cct | tgg | agc | agt | gct | gga | agt | act | gtg | tgg | agg | aac | aga | gag | acg | 2197 |
| Leu | Pro | Trp | Ser | Ser | Ala | Gly | Ser | Thr | Val | Trp | Arg | Asn | Arg | Glu | Thr | |
| | | | | 415 | | | | | 420 | | | | | 425 | | |
| tta | atg | gag | ttt | gag | gaa | cca | cac | gcc | acg | aag | cag | tct | gtg | ata | gca | 2245 |
| Leu | Met | Glu | Phe | Glu | Glu | Pro | His | Ala | Thr | Lys | Gln | Ser | Val | Ile | Ala | |
| | | | | 430 | | | | | 435 | | | | | 440 | | |
| 445 | | | | | | | | | | | | | | | | |
| ttg | ggc | tca | caa | gag | gga | gct | ctg | cat | caa | gct | ttg | gct | gga | gcc | att | 2293 |
| Leu | Gly | Ser | Gln | Glu | Gly | Ala | Leu | His | Gln | Ala | Leu | Ala | Gly | Ala | Ile | |
| | | | | 450 | | | | | 455 | | | | | 460 | | |
| cct | gtg | gaa | ttt | tca | agc | aac | act | gtc | aag | ttg | acg | tcg | ggt | cat | ttg | 2341 |
| Pro | Val | Glu | Phe | Ser | Ser | Asn | Thr | Val | Lys | Leu | Thr | Ser | Gly | His | Leu | |
| | | | | 465 | | | | | 470 | | | | | 475 | | |
| aag | tgt | aga | gtg | aag | atg | gaa | aaa | ttg | cag | ttg | aag | gga | aca | acc | tat | 2389 |
| Lys | Cys | Arg | Val | Lys | Met | Glu | Lys | Leu | Gln | Leu | Lys | Gly | Thr | Thr | Tyr | |
| | | | | 480 | | | | | 485 | | | | | 490 | | |
| ggc | gtc | tgt | tca | aag | gct | ttc | aag | ttt | ctt | ggg | act | ccc | gcg | gac | aca | 2437 |
| Gly | Val | Cys | Ser | Lys | Ala | Phe | Lys | Phe | Leu | Gly | Thr | Pro | Ala | Asp | Thr | |
| | | | | 495 | | | | | 500 | | | | | 505 | | |
| ggt | cac | ggc | act | gtg | gtg | ttg | gaa | ttg | cag | tac | act | ggc | acg | gat | gga | 2485 |
| Gly | His | Gly | Thr | Val | Val | Leu | Glu | Leu | Gln | Tyr | Thr | Gly | Thr | Asp | Gly | |
| | | | | 510 | | | | | 515 | | | | | 520 | | |
| 525 | | | | | | | | | | | | | | | | |
| cct | tgc | aaa | gtt | cct | atc | tcg | tca | gtg | gct | tca | ttg | aac | gac | cta | acg | 2533 |
| Pro | Cys | Lys | Val | Pro | Ile | Ser | Ser | Val | Ala | Ser | Leu | Asn | Asp | Leu | Thr | |
| | | | | 530 | | | | | 535 | | | | | 540 | | |
| cca | gtg | ggc | aga | ttg | gtc | act | gtc | aac | cct | ttt | gtt | tca | gtg | gcc | acg | 2581 |
| Pro | Val | Gly | Arg | Leu | Val | Thr | Val | Asn | Pro | Phe | Val | Ser | Val | Ala | Thr | |
| | | | | 545 | | | | | 550 | | | | | 555 | | |
| gcc | aac | gct | aag | gtc | ctg | att | gaa | ttg | gaa | cca | ccc | ttt | gga | gac | tca | 2629 |
| Ala | Asn | Ala | Lys | Val | Leu | Ile | Glu | Leu | Glu | Pro | Pro | Phe | Gly | Asp | Ser | |
| | | | | 560 | | | | | 565 | | | | | 570 | | |
| tac | ata | gtg | gtg | ggc | aga | gga | gaa | caa | cag | atc | aat | cac | cat | tgg | cac | 2677 |
| Tyr | Ile | Val | Val | Gly | Arg | Gly | Glu | Gln | Gln | Ile | Asn | His | His | Trp | His | |
| | | | | 575 | | | | | 580 | | | | | 585 | | |

aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga 2725
Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly
590 595 600 605

gcg cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca 2773
Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser
610 615 620

gtt gga ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc 2821
Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe
625 630 635

gga gga gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa 2869
Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln
640 645 650

gga ttg ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat 2917
Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp
655 660 665

agg tcc ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc 2965
Arg Ser Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe
670 675 680 685

ctc tcc gtg aac gtg cac gcc t gaaggcggcc gctcagacat gcatctagag 3017
Leu Ser Val Asn Val His Ala
690

ggccctattc tatagtgtca cctaaatgct agagctcgct gatcagcctc gactgtgcct 3077
tctagttgcc agccatctgt tgtttgcccc tccccgtgc cttccttgac cctggaaggt 3137
gccactccca ctgtcctttc ctaataaaat gaggaattg catcgcatg tctgagtagg 3197
tgtcattcta ttctgggggg tggggtgggg caggacagca agggggagga ttgggaagac 3257
aatagcaggc atgctgggga tgcggtgggc tctatggctt ctgaggcgga aagaaccagc 3317
tgcattaatg aatcggccaa cgcgcgggga gaggcgggtt gcgtattggg cgctcttccg 3377
cttcctcgct cactgactcg ctgcgctcgg tcggtcggct gcggcgagcg gtatcagctc 3437
actcaaaggc ggtaatacgg ttatccacag aatcagggga taacgcagga aagaacatgt 3497
gagcaaaagg ccagcaaaag gccaggaacc gtaaaaaggc cgcgttgctg gcgtttttcc 3557
ataggctccg cccccctgac gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa 3617
acccgacagg actataaaga taccaggcgt ttccccctgg aagctccctc gtgcgctctc 3677
ctgttccgac cctgcgcgtt accggatacc tgtccgcctt tctcccttcg ggaagcgtgg 3737
cgctttctca tagctcacgc tgtaggtatc tcagttcggg taggtcgtt cgctccaagc 3797
tgggctgtgt gcacgaaccc cccgttcagc ccgaccgctg cgccttatcc ggtaactatc 3857
gtcttgagtc caaccggta agacacgact tatcgccact ggcagcagcc actggttaaca 3917
ggattagcag agcagggatg gtaggcgggtg ctacagagtt cttgaagtgg tggcctaact 3977
acggctacac tagaagaaca gtatttggtg tctgcgctct gctgaagcca gttaccttcg 4037
gaaaaagagt tggtagctct tgatccggca aacaaaccac cgctggtagc ggtggttttt 4097
ttgtttgcaa gcagcagatt acgcgcagaa aaaaaggatc tcaagaagat cctttgatct 4157
tttctacggg gtctgacgct cagtggaaacg aaaactcacg ttaagggatt ttggtcatga 4217
gattatcaaa aaggatcttc acctagatcc ttttaaatta aaaatgaagt tttaaatcaa 4277
tctaaagtat atatgagtaa acttggtctg acagttacca atgcttaatc agtgaggcac 4337
ctatctcagc gatctgtcta tttcgttcat ccatagttgc ctgactcccc gtcgtgtaga 4397
taactacgat acgggagggc ttaccatctg gccccagtgc tgcaatgata ccgcgagacc 4457
cacgctcacc ggctccagat ttatcagcaa taaaccagcc agccggaagg gccgagcgca 4517


```

gaagtgggtcc tgcaacttta tccgcctcca tccagtctat taattgttgc cgggaagcta 4577
gagtaagtag ttgccaggtt aatagtttgc gcaacgttgt tgccattgct acaggcatcg 4637
tggtgtcacg ctcgctgttt ggtatggctt cattcagctc cggttcccaa cgatcaaggc 4697
gagttacatg atcccccatg ttgtgcaaaa aagcgggttag ctccctcggt cctccgatcg 4757
ttgtcagaag taagttggcc gcagtgttat cactcatggt tatggcagca ctgcataatt 4817
ctcttactgt catgccatcc gtaagatgct tttctgtgac tggtgagtac tcaaccaagt 4877
cattctgaga atagtgtatg cggcgaccga gttgctcttg cccggcgtca atacgggata 4937
ataccgcgcc acatagcaga actttaaaag tgctcatcat tggaaaacgt tcttcggggc 4997
gaaaactctc aaggatctta ccgctgttga gatccagttc gatgtaacct actcgtgcac 5057
ccaactgata ttcagcatct tttactttca ccagcgtttc tgggtgagca aaaacaggaa 5117
ggcaaaatgc cgcaaaaaag ggaataaggg cgacacggaa atgttgaata ctcatactct 5177
tcctttttca atattattga agcattttatc agggttattg tctcatgagc ggatacatat 5237
ttgaatgtat ttagaaaaat aaacaaatag gggttccgcg cacatttccc cgaaaagtgc 5297
cacctgacgt c 5308

```

<210> 16

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCBWN

<400> 16

```

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1           5           10           15
Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
          20           25           30
Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
          35           40           45
Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
          50           55           60
Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
65           70           75           80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
          85           90           95
Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
          100          105          110
Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
          115          120          125
Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
          130          135          140
Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
145          150          155          160
Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg
          165          170          175
Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe
          180          185          190
Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly
          195          200          205

```

Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile
210 215 220
Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu
225 230 235 240
Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val
245 250 255
Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His
260 265 270
Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val
275 280 285
Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
290 295 300
Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr
305 310 315 320
Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
325 330 335
Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala
340 345 350
Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr
355 360 365
Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg
370 375 380
Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys
385 390 395 400
Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp
405 410 415
Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu
420 425 430
Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser
435 440 445
Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu
450 455 460
Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
465 470 475 480
Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys
485 490 495
Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly
500 505 510
Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys
515 520 525
Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly
530 535 540
Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala
545 550 555 560
Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
565 570 575
Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly
580 585 590
Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg
595 600 605
Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
610 615 620
Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625 630 635 640

14114.0332U3

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
645 650 655
Gly Ala Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile
660 665 670
Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val
675 680 685
Asn Val His Ala
690

<210> 17
<211> 5334
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> CDS
<222> (916)...(3007)
<221> misc_feature
<222> (1)...(5334)
<223> pCBE 1-14

<400> 17
gacggatcgg gagatctccc gatcccttat ggtgcactct cagtacaatc tgctctgatg 60
ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgt gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggttag gcgttttgcg ctgcttcgag atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagtcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggag tatttacggt aaactgcca cttggcagta catcaagtgt 480
atcatatgcc aagtacgcc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
atgccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca 600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg 780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca 840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagaccaa gcttggtacc 900
tctagagccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa 951
Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
1 5 10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg 999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
15 20 25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc 1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
30 35 40

1047: 5334

| | |
|---|------|
| aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga | 1095 |
| Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly | |
| 45 50 55 60 | |
| gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag | 1143 |
| Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu | |
| 65 70 75 | |
| gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca | 1191 |
| Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro | |
| 80 85 90 | |
| gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat | 1239 |
| Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr | |
| 95 100 105 | |
| gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg | 1287 |
| Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val | |
| 110 115 120 | |
| tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct | 1335 |
| Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala | |
| 125 130 135 140 | |
| tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac | 1383 |
| Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn | |
| 145 150 155 | |
| tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc | 1431 |
| Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly | |
| 160 165 170 | |
| tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc | 1479 |
| Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu | |
| 175 180 185 | |
| ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc | 1527 |
| Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly | |
| 190 195 200 | |
| aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg | 1575 |
| Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu | |
| 205 210 215 220 | |
| gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca | 1623 |
| Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro | |
| 225 230 235 | |
| aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag | 1671 |
| Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu | |
| 240 245 250 | |
| gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg | 1719 |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Val | Arg | Ser | Tyr | Cys | Tyr | His | Ala | Ser | Val | Thr | Asp | Ile | Ser | Thr | Val | | |
| | 255 | | | | | | 260 | | | | | 265 | | | | | |
| gct | cgg | tgc | ccc | acg | act | gga | gaa | gcc | cac | aac | gag | aag | cga | gct | gat | 1767 | |
| Ala | Arg | Cys | Pro | Thr | Thr | Gly | Glu | Ala | His | Asn | Glu | Lys | Arg | Ala | Asp | | |
| | 270 | | | | | 275 | | | | | 280 | | | | | | |
| agt | agc | tat | gtg | tgc | aaa | caa | ggc | ttc | act | gac | cgt | ggg | tgg | ggc | aac | 1815 | |
| Ser | Ser | Tyr | Val | Cys | Lys | Gln | Gly | Phe | Thr | Asp | Arg | Gly | Trp | Gly | Asn | | |
| 285 | | | | | 290 | | | | | 295 | | | | | 300 | | |
| gga | tgt | gga | ctt | ttc | ggg | aag | gga | agc | att | gac | aca | tgt | gca | aaa | ttc | 1863 | |
| Gly | Cys | Gly | Leu | Phe | Gly | Lys | Gly | Ser | Ile | Asp | Thr | Cys | Ala | Lys | Phe | | |
| | | | | 305 | | | | | 310 | | | | | 315 | | | |
| tcc | tgc | acc | agt | aaa | gcg | att | ggg | aga | aca | atc | cag | cca | gaa | aac | atc | 1911 | |
| Ser | Cys | Thr | Ser | Lys | Ala | Ile | Gly | Arg | Thr | Ile | Gln | Pro | Glu | Asn | Ile | | |
| | | | 320 | | | | | 325 | | | | | 330 | | | | |
| aaa | tac | gaa | gtt | ggc | att | ttt | gtg | cat | gga | acc | acc | act | tcg | gaa | aac | 1959 | |
| Lys | Tyr | Glu | Val | Gly | Ile | Phe | Val | His | Gly | Thr | Thr | Thr | Ser | Glu | Asn | | |
| | | 335 | | | | | 340 | | | | | | 345 | | | | |
| cat | ggg | aat | tat | tca | gcg | caa | gtt | ggg | gcg | tcc | cag | gcg | gca | aag | ttt | 2007 | |
| His | Gly | Asn | Tyr | Ser | Ala | Gln | Val | Gly | Ala | Ser | Gln | Ala | Ala | Lys | Phe | | |
| | 350 | | | | | 355 | | | | | 360 | | | | | | |
| aca | gta | aca | ccc | aat | gct | cct | tcg | ata | acc | ctc | aaa | ctt | ggt | gac | tac | 2055 | |
| Thr | Val | Thr | Pro | Asn | Ala | Pro | Ser | Ile | Thr | Leu | Lys | Leu | Gly | Asp | Tyr | | |
| | 365 | | | | 370 | | | | | 375 | | | | | 380 | | |
| gga | gaa | gtc | aca | ctg | gac | tgt | gag | cca | agg | agt | gga | ctg | aac | act | gaa | 2103 | |
| Gly | Glu | Val | Thr | Leu | Asp | Cys | Glu | Pro | Arg | Ser | Gly | Leu | Asn | Thr | Glu | | |
| | | | | 385 | | | | 390 | | | | | | 395 | | | |
| gcg | ttt | tac | gtc | atg | acc | gtg | ggg | tca | aag | tca | ttt | ctg | gtc | cat | agg | 2151 | |
| Ala | Phe | Tyr | Val | Met | Thr | Val | Gly | Ser | Lys | Ser | Phe | Leu | Val | His | Arg | | |
| | | | 400 | | | | | 405 | | | | | 410 | | | | |
| gag | tgg | ttt | cat | gac | ctc | gct | ctc | ccc | tgg | acg | tcc | cct | tcg | agc | aca | 2199 | |
| Glu | Trp | Phe | His | Asp | Leu | Ala | Leu | Pro | Trp | Thr | Ser | Pro | Ser | Ser | Thr | | |
| | | 415 | | | | | 420 | | | | | 425 | | | | | |
| gcg | tgg | aga | aac | aga | gaa | ctc | ctc | atg | gaa | ttt | gaa | gag | gcg | cac | gcc | 2247 | |
| Ala | Trp | Arg | Asn | Arg | Glu | Leu | Leu | Met | Glu | Phe | Glu | Glu | Ala | His | Ala | | |
| | | 430 | | | | 435 | | | | | 440 | | | | | | |
| aca | aaa | cag | tcc | gtt | gtt | gct | ctt | ggg | tca | cag | gaa | gga | ggc | ctc | cat | 2295 | |
| Thr | Lys | Gln | Ser | Val | Val | Ala | Leu | Gly | Ser | Gln | Glu | Gly | Gly | Leu | His | | |
| | | | | 445 | | 450 | | | | 455 | | | | | 460 | | |
| cag | gcg | ttg | gca | gga | gcc | atc | gtg | gtg | gag | tac | tca | agc | tca | gtg | aag | 2343 | |
| Gln | Ala | Leu | Ala | Gly | Ala | Ile | Val | Val | Glu | Tyr | Ser | Ser | Ser | Val | Lys | | |
| | | | | 465 | | | | 470 | | | | | | 475 | | | |

14114.0332U3

| | |
|--|------|
| tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct | 2391 |
| Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala | |
| 480 485 490 | |
| ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg | 2439 |
| Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala | |
| 495 500 505 | |
| aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc | 2487 |
| Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser | |
| 510 515 520 | |
| tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg | 2535 |
| Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala | |
| 525 530 535 540 | |
| agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc | 2583 |
| Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro | |
| 545 550 555 | |
| ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa | 2631 |
| Phe Val Ala Thr Ser Ser Ala Ser Lys Val Leu Val Glu Met Glu | |
| 560 565 570 | |
| ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag | 2679 |
| Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln | |
| 575 580 585 | |
| atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt | 2727 |
| Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe | |
| 590 595 600 | |
| tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca | 2775 |
| Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr | |
| 605 610 615 620 | |
| gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa | 2823 |
| Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys | |
| 625 630 635 | |
| gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga | 2871 |
| Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly | |
| 640 645 650 | |
| atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg | 2919 |
| Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met | |
| 655 660 665 | |
| ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca | 2967 |
| Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr | |
| 670 675 680 | |
| ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct t aattagtttg | 3017 |

2025 RELEASE UNDER E.O. 14176

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
685 690 695

```

agcggccgct cgagcatgca tctagagggc cctattctat agtgtcacct aaatgctaga 3077
gctcgctgat cagcctcgac tgtgccttct agttgccagc catctgttgt ttgcccctcc 3137
cccgtgcctt ccttgaccct ggaaggtgcc actcccactg tcccttccta ataaaatgag 3197
gaaattgcat cgcattgtct gagtaggtgt cattctatct tgggggggtgg ggtggggcag 3257
gacagcaagg gggaggattg ggaagacaat agcaggcatg ctgggggatgc ggtgggctct 3317
atggcttctg aggcggaaaag aaccagctgc attaatgaat cggccaacgc gcggggagag 3377
gcggtttgcg tattggggcg tcttcgctt cctcgctcac tgactcgctg cgctcggctc 3437
ttcggctgcg gcgagcggta tcagctcact caaaggcggg aatacgggta tccacagaat 3497
caggggataa cgcaggaaaag aacatgtgag caaaaggcca gcaaaaggcc aggaaccgta 3557
aaaaggccgc gttgctggcg tttttccata ggctccgcc ccctgacgag catcacaaaa 3617
atcgacgctc aagtcagagg tggcgaaaacc cgacaggact ataaagatac caggcgtttc 3677
cccctggaag ctccctcgct cgctctcctg ttcgaccct gccgcttacc ggatacctgt 3737
ccgcctttct ccttcggga agcgtggcg tttctcatag ctcacgctgt aggtatctca 3797
gttcggtgta ggtcgctgc tccaagctgg gctgtgtgca cgaaccccc gttcagccc 3857
accgctgcgc cttatccggg aactatcgct ttgagtccaa cccggtgaaga cagacttat 3917
cgccactggc agcagccact ggtaacagga ttagcagagc gaggtatgta ggcgggtgcta 3977
cagagttctt gaagtgggtg cctaactacg gctacactag aagaacagta tttggtatct 4037
gcgctctgct gaagccagtt accttcggaa aaagagttgg tagctcttga tccggcaaac 4097
aaaccaccgc tggtagcggg ggtttttttg tttgcaagca gcagattacg cgcaaaaaa 4157
aaggatctca agaagatcct ttgatctttt ctacggggtc tgacgctcag tggaacgaaa 4217
actcacgtta agggattttg gtcatgagat tatcaaaaag gatcttcacc tagatcctt 4277
taaattaaaa atgaagtttt aaatcaatct aaagtatata tgagtaaact tggctgaca 4337
gttaccaatg cttaatcagt gaggcaccta tctcagcgat ctgtctatct cgctcatcca 4397
tagttgcctg actccccgtc gtgtagataa ctacgatacg ggagggttta ccatctggcc 4457
ccagtgcctg aatgataccg cgagacccac gctcacccgc tccagattta tcagcaataa 4517
accagccagc cggaaggggc gagcgcagaa gtgggtcctgc aactttatcc gcctccatcc 4577
agtctattaa ttgttgccgg gaagctagag taagtagttc gccagttaat agtttgcgca 4637
acgttggtgc cattgctaca ggcacgtgg tgtcacgctc gtcgtttggg atggcttcat 4697
tcagctccgg ttcccaacga tcaaggcgag ttacatgac ccccatgttg tgcaaaaaa 4757
cggttagctc cttcggctct ccgacgttg tcagaagtaa gttggccgca gtgttatcac 4817
tcatgggtat ggcagcactg cataattctc ttactgtcat gccatccgta agatgctttt 4877
ctgtgactgg tgagtactca accaagtcac totgagaata gtgtatgcgg cgaccgagtt 4937
gctcttgccc ggcgtcaata cgggataata ccgcgccaca tagcagaact ttaaaagtgc 4997
tcacattggg aaaacgttct tcggggcgaa aactctcaag gatcttaccg ctgttgagat 5057
ccagttcgat gtaaccact cgtgcaccca actgatcttc agcatctttt actttcacca 5117
gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga ataaggcgca 5177
cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg 5237
gttattgtct catgagcgga tacatatctg aatgtattta gaaaaataaa caaatagggg 5297
ttccgcgcac atttccccga aaagtgccac ctgacgt 5334

```

<210> 18

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCBE 1-14

ATTORNEY DOCKET NO. 14114.0332U3

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Lys | Gln | Asn | Lys | Arg | Gly | Gly | Asn | Glu | Gly | Ser | Ile | Met |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Trp | Leu | Ala | Ser | Leu | Ala | Val | Val | Ile | Ala | Cys | Ala | Gly | Ala | Met | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Ser | Asn | Phe | Gln | Gly | Lys | Leu | Leu | Met | Thr | Ile | Asn | Asn | Thr | Asp |
| | | | 35 | | | | | 40 | | | | 45 | | | |
| Ile | Ala | Asp | Val | Ile | Val | Ile | Pro | Thr | Ser | Lys | Gly | Glu | Asn | Arg | Cys |
| | | | 50 | | | | | 55 | | | | 60 | | | |
| Trp | Val | Arg | Ala | Ile | Asp | Val | Gly | Tyr | Met | Cys | Glu | Asp | Thr | Ile | Thr |
| 65 | | | | | | | | | | | | | | | |
| Tyr | Glu | Cys | Pro | Lys | Leu | Thr | Met | Gly | Asn | Asp | Pro | Glu | Asp | Val | Asp |
| | | | | 85 | | | | | | | | | | 95 | |
| Cys | Trp | Cys | Asp | Asn | Gln | Glu | Val | Tyr | Val | Gln | Tyr | Gly | Arg | Cys | Thr |
| | | | | 100 | | | | | | | | | | | |
| Arg | Thr | Arg | His | Ser | Lys | Arg | Ser | Arg | Arg | Ser | Val | Ser | Val | Gln | Thr |
| | | | | | | | | | | | | | | | |
| His | Gly | Glu | Ser | Ser | Leu | Val | Asn | Lys | Lys | Glu | Ala | Trp | Leu | Asp | Ser |
| | | | | | | | | | | | | | | | |
| Thr | Lys | Ala | Thr | Arg | Tyr | Leu | Met | Lys | Thr | Glu | Asn | Trp | Ile | Ile | Arg |
| 145 | | | | | | | | | | | | | | | |
| Asn | Pro | Gly | Tyr | Ala | Phe | Leu | Ala | Ala | Val | Leu | Gly | Trp | Met | Leu | Gly |
| | | | | | | | | | | | | | | | |
| Ser | Asn | Asn | Gly | Gln | Arg | Val | Val | Phe | Thr | Ile | Leu | Leu | Leu | Leu | Val |
| | | | | | | | | | | | | | | | |
| Ala | Pro | Ala | Tyr | Ser | Phe | Asn | Cys | Leu | Gly | Met | Gly | Asn | Arg | Asp | Phe |
| | | | | | | | | | | | | | | | |
| Ile | Glu | Gly | Ala | Ser | Gly | Ala | Thr | Trp | Val | Asp | Leu | Val | Leu | Glu | Gly |
| | | | | | | | | | | | | | | | |
| Asp | Ser | Cys | Leu | Thr | Ile | Met | Ala | Asn | Asp | Lys | Pro | Thr | Leu | Asp | Val |
| 225 | | | | | | | | | | | | | | | |
| Arg | Met | Ile | Asn | Ile | Glu | Ala | Ser | Gln | Leu | Ala | Glu | Val | Arg | Ser | Tyr |
| | | | | | | | | | | | | | | | |
| Cys | Tyr | His | Ala | Ser | Val | Thr | Asp | Ile | Ser | Thr | Val | Ala | Arg | Cys | Pro |
| | | | | | | | | | | | | | | | |
| Thr | Thr | Gly | Glu | Ala | His | Asn | Glu | Lys | Arg | Ala | Asp | Ser | Ser | Tyr | Val |
| | | | | | | | | | | | | | | | |
| Cys | Lys | Gln | Gly | Phe | Thr | Asp | Arg | Gly | Trp | Gly | Asn | Gly | Cys | Gly | Leu |
| | | | | | | | | | | | | | | | |
| Phe | Gly | Lys | Gly | Ser | Ile | Asp | Thr | Cys | Ala | Lys | Phe | Ser | Cys | Thr | Ser |
| 305 | | | | | | | | | | | | | | | |
| Lys | Ala | Ile | Gly | Arg | Thr | Ile | Gln | Pro | Glu | Asn | Ile | Lys | Tyr | Glu | Val |
| | | | | | | | | | | | | | | | |
| Gly | Ile | Phe | Val | His | Gly | Thr | Thr | Thr | Ser | Glu | Asn | His | Gly | Asn | Tyr |
| | | | | | | | | | | | | | | | |
| Ser | Ala | Gln | Val | Gly | Ala | Ser | Gln | Ala | Ala | Lys | Phe | Thr | Val | Thr | Pro |
| | | | | | | | | | | | | | | | |
| Asn | Ala | Pro | Ser | Ile | Thr | Leu | Lys | Leu | Gly | | | | | | |

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
 420 425 430
 Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
 435 440 445
 Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
 450 455 460
 Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
 465 470 475 480
 His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
 485 490 495
 Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
 500 505 510
 Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
 515 520 525
 Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
 530 535 540
 Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
 545 550 555 560
 Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
 565 570 575
 Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
 580 585 590
 Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
 595 600 605
 Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
 610 615 620
 Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
 625 630 635 640
 Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
 645 650 655
 Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
 660 665 670
 Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
 675 680 685
 Val Phe Leu Ala Thr Asn Val His Ala
 690 695

<210> 19

<211> 5283

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<221> CDS

<222> (910)...(2965)

<400> 19

| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|-----|
| gacggatcgg | gagatctccc | gatcccttat | ggtcgactct | cagtacaatc | tgctctgatg | 60 |
| ccgcatagtt | aagccagtat | ctgctccctg | cttgtgtgtt | ggaggtcgct | gagtagtgcg | 120 |
| cgagcaaaat | ttaagctaca | acaaggcaag | gcttgaccga | caattgcatg | aagaatctgc | 180 |
| ttaggggttag | gcggttttgcg | ctgcttcgcg | atgtacgggc | cagatatacg | cgttgacatt | 240 |

gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata 300
 tggagtccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
 attgacgtca atgggtggac tatttacggg aaactgcccc cttggcagta catcaagtgt 480
 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
 atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600
 tcgctattac catgggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
 actcacggggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780
 gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca 840
 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc 900
 gccgcccgc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
 1 5 10

ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cgg gac 999
 Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp
 15 20 25 30

agg gaa gga tac atg gtt atg cgg gcc agt gga agg gac gct gca agc 1047
 Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser
 35 40 45

cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg 1095
 Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met
 50 55 60

gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac 1143
 Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp
 65 70 75

cag gag gaa gaa ccc gtt gac gtg gac tgc ttc tgc cga ggt gtt gat 1191
 Gln Glu Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp
 80 85 90

agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg 1239
 Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg
 95 100 105 110

ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc 1287
 Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val
 115 120 125

ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc 1335
 Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val
 130 135 140

acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc 1383
 Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala
 145 150 155

att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg 1431
 Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val
 160 165 170

T-000000-000000

act gtc atc ctc ttg gcg ttg agt cta ggg cca gtg tac gcc acg agg 1479
 Thr Val Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg
 175 180 185 190

tgc acg cat ctt gag aac aga gat ttt gtg aca gga act caa ggg acc 1527
 Cys Thr His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr
 195 200 205

acc aga gtg tcc cta gtt ttg gaa ctt gga ggc tgc gtg acc atc aca 1575
 Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr
 210 215 220

gct gag ggc aag cca tcc att gat gta tgg ctc gaa gac att ttt cag 1623
 Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln
 225 230 235

gaa agc ccg gct gaa acc aga gaa tac tgc ctg cac gcc aaa ttg acc 1671
 Glu Ser Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr
 240 245 250

aac aca aaa gtg gag gct cgc tgt cca acc act gga ccg gcg aca ctt 1719
 Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu
 255 260 265 270

ccg gag gag cat cag gct aat atg gtg tgc aag aga gac caa agc gac 1767
 Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp
 275 280 285

cgt gga tgg gga aac cac tgc ggg ttt ttt ggg aag ggc agt ata gtg 1815
 Arg Gly Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val
 290 295 300

gct tgt gca aag ttt gaa tgc gag gaa gca aaa aaa gct gtg ggc cac 1863
 Ala Cys Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His
 305 310 315

gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac 1911
 Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His
 320 325 330

aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca 1959
 Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser
 335 340 345 350

gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac 2007
 Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp
 355 360 365

tat gga gat gtg tcg ctg acg tgt aaa gtg gca agt ggg att gat gtc 2055
 Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val
 370 375 380

gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct 2103

14114.0332U3

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Ala | Gln | Thr | Val | Val | Met | Ser | Leu | Asp | Ser | Ser | Lys | Asp | His | Leu | Pro | | |
| | | | 385 | | | | 390 | | | | | 395 | | | | | |
| tct | gca | tgg | caa | gtg | cac | cgt | gac | tgg | ttt | gag | gac | ttg | gcg | ctg | ccc | 2151 | |
| Ser | Ala | Trp | Gln | Val | His | Arg | Asp | Trp | Phe | Glu | Asp | Leu | Ala | Leu | Pro | | |
| | 400 | | | | | 405 | | | | | 410 | | | | | | |
| tgg | aaa | cac | aag | gac | aac | caa | gat | tgg | aac | agt | gtg | gag | aaa | ctt | gtg | 2199 | |
| Trp | Lys | His | Lys | Asp | Asn | Gln | Asp | Trp | Asn | Ser | Val | Glu | Lys | Leu | Val | | |
| 415 | | | | | 420 | | | | | 425 | | | | | 430 | | |
| gaa | ttt | gga | cca | cca | cat | gct | gtg | aaa | atg | gat | gtt | ttc | aat | ctg | ggg | 2247 | |
| Glu | Phe | Gly | Pro | Pro | His | Ala | Val | Lys | Met | Asp | Val | Phe | Asn | Leu | Gly | | |
| | | | | 435 | | | | | 440 | | | | | 445 | | | |
| gac | cag | acg | gct | gtg | ctg | ctc | aaa | tca | ctg | gca | gga | gtt | ccg | ctg | gcc | 2295 | |
| Asp | Gln | Thr | Ala | Val | Leu | Leu | Lys | Ser | Leu | Ala | Gly | Val | Pro | Leu | Ala | | |
| | | | 450 | | | | | 455 | | | | | 460 | | | | |
| agt | gtg | gag | ggc | cag | aaa | tac | cac | ctg | aaa | agc | ggc | cat | gtt | act | tgt | 2343 | |
| Ser | Val | Glu | Gly | Gln | Lys | Tyr | His | Leu | Lys | Ser | Gly | His | Val | Thr | Cys | | |
| | 465 | | | | | | 470 | | | | | 475 | | | | | |
| gat | gtg | gga | ctg | gaa | aag | ctg | aaa | ctg | aaa | ggc | aca | acc | tac | tcc | atg | 2391 | |
| Asp | Val | Gly | Leu | Glu | Lys | Leu | Lys | Leu | Lys | Gly | Thr | Thr | Tyr | Ser | Met | | |
| | 480 | | | | | 485 | | | | | 490 | | | | | | |
| tgt | gac | aaa | gca | aag | ttc | aaa | tgg | aag | aga | gtt | cct | gtg | gac | agc | ggc | 2439 | |
| Cys | Asp | Lys | Ala | Lys | Phe | Lys | Trp | Lys | Arg | Val | Pro | Val | Asp | Ser | Gly | | |
| 495 | | | | | 500 | | | | | 505 | | | | | 510 | | |
| cat | gac | aca | gta | gtc | atg | gag | gta | tca | tac | aca | gga | agc | gac | aag | cca | 2487 | |
| His | Asp | Thr | Val | Val | Met | Glu | Val | Ser | Tyr | Thr | Gly | Ser | Asp | Lys | Pro | | |
| | | | | 515 | | | | | 520 | | | | | 525 | | | |
| tgt | cgg | atc | ccg | gtg | cgg | gct | gtg | gca | cat | ggg | gtc | cca | gcg | gtt | aat | 2535 | |
| Cys | Arg | Ile | Pro | Val | Arg | Ala | Val | Ala | His | Gly | Val | Pro | Ala | Val | Asn | | |
| | | | 530 | | | | | 535 | | | | | 540 | | | | |
| gta | gcc | atg | ctc | ata | acc | ccc | aat | cca | acc | att | gaa | aca | aat | ggg | ggc | 2583 | |
| Val | Ala | Met | Leu | Ile | Thr | Pro | Asn | Pro | Thr | Ile | Glu | Thr | Asn | Gly | Gly | | |
| | | 545 | | | | | 550 | | | | | 555 | | | | | |
| gga | ttc | ata | gaa | atg | cag | ctg | cca | cca | ggg | gat | aac | atc | atc | tat | gtg | 2631 | |
| Gly | Phe | Ile | Glu | Met | Gln | Leu | Pro | Pro | Gly | Asp | Asn | Ile | Ile | Tyr | Val | | |
| | 560 | | | | | 565 | | | | | 570 | | | | | | |
| gga | gac | ctt | agc | cag | cag | tgg | ttt | cag | aaa | ggc | agt | acc | att | ggg | aga | 2679 | |
| Gly | Asp | Leu | Ser | Gln | Gln | Trp | Phe | Gln | Lys | Gly | Ser | Thr | Ile | Gly | Arg | | |
| 575 | | | | | 580 | | | | | 585 | | | | | 590 | | |
| atg | ttt | gaa | aaa | acc | cgc | agg | gga | ttg | gaa | agg | ctc | tct | gtg | gtt | gga | 2727 | |
| Met | Phe | Glu | Lys | Thr | Arg | Arg | Gly | Leu | Glu | Arg | Leu | Ser | Val | Val | Gly | | |
| | | | | 595 | | | | 600 | | | | | | 605 | | | |

2025-04-23 14:33:50

| | |
|--|------|
| gaa cat gca tgg gac ttt ggc tca gta ggc ggg gta ctg tct tct gtg | 2775 |
| Glu His Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val | |
| 610 615 620 | |
| ggg aag gca atc cac acg gtg ctg ggg gga gct ttc aac acc ctt ttt | 2823 |
| Gly Lys Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe | |
| 625 630 635 | |
| ggg ggg gtt gga ttc atc cct aag atg ctg ctg ggg gtt gct ctg gtc | 2871 |
| Gly Gly Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val | |
| 640 645 650 | |
| tgg ttg gga cta aat gcc agg aat cca acg atg tcc atg acg ttt ctt | 2919 |
| Trp Leu Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu | |
| 655 660 665 670 | |
| gct gtg ggg gct ttg aca ctg atg atg aca atg gga gtt ggg gca t | 2965 |
| Ala Val Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala | |
| 675 680 685 | |
| gagcggccgc tcgagcatgc atctagaggg ccctatttcta tagtgtcacc taaatgctag | 3025 |
| agctcgctga tcagcctcga ctgtgccttc tagttgccag ccactctgtt tttgccctc | 3085 |
| ccccgtgcct tccttgacct tggaagggtgc cactccact gtcctttcct aataaaatga | 3145 |
| ggaaattgca tcgcattgtc tgagtaggtg tcatttctatt ctgggggggtg ggggtggggca | 3205 |
| ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctggggatg cgggtgggctc | 3265 |
| tatggcttct gaggcggaaa gaacagctgc attaatgaat cggccaacgc gcggggagag | 3325 |
| gcggtttgcg tattgggcgc tcttcgcctt cctcgctcac tgactcgctg cgctcggtcg | 3385 |
| ttcggtcgcg gcgagcggta tcagctcact caaaggcggg aatacggtta tccacagaat | 3445 |
| caggggataa cgcaggaaa aacatgtgag caaaaggcca gcaaaaggcc aggaaccgta | 3505 |
| aaaaggccgc gttgctggcg tttttccata ggctccgccc ccctgacgag catcacaaaa | 3565 |
| atcgacgctc aagtcagagg tggcgaaaacc cgacaggact ataaagatac caggcgtttc | 3625 |
| cccctggaag ctccctcggt cgcctctctg ttcgcaccct gccgcttacc ggatacctgt | 3685 |
| ccgcctttct ccttcggga agcgtggcgc tttctcaatg ctcacgctgt aggtatctca | 3745 |
| gttcggtgta ggtcggtgcg tccaagctgg gctgtgtgca cgaaccccc gttcagccc | 3805 |
| accgctgcgc cttatccggt aactatcgct ttgagtccaa cccggttaaga cacgacttat | 3865 |
| cgccactggc agcagccact ggtaacagga ttagcagagc gaggtatgta ggcggtgcta | 3925 |
| cagagttcct gaagtgggtg cctaactacg gctacactag aaggacagta tttggtatct | 3985 |
| gcgctctgct gaagccagtt accttcggaa aaagagttgg tagctcttga tccggcaaac | 4045 |
| aaaccaccgc tggtagcggg ggtttttttt tttgcaagca gcagattacg cgcagaaaaa | 4105 |
| aaggatctca agaagatcct ttgatctttt ctacggggtc tgacgctcag tggaacgaaa | 4165 |
| actcacgtta agggattttg gtcatgagat tatcaaaaag gatcttcacc tagatccttt | 4225 |
| taaattaaaa atgaagtttt aaatcaatct aaagtatata tgagtaaaact tggcttgaca | 4285 |
| gttaccaatg cttaatcagt gaggcaccta tctcagcgat ctgtctattt cgttcatcca | 4345 |
| tagttgcctg actcccgtc gtgtagataa ctacgatacg ggagggctta ccatctggcc | 4405 |
| ccagtgctgc aatgataccg cgagaccac gctcacggc tccagattta tcagcaataa | 4465 |
| accagccagc cggaagggcc gagcgcagaa gtggtcctgc aactttatcc gcctccatcc | 4525 |
| agtctattaa ttggtgccgg gaagctagag taagtagttc gccagttaat agtttgcgca | 4585 |
| acgttgttgc cattgctaca ggcacgtgg tgtcacgctc gtcgtttggt atggcttcac | 4645 |
| tcagctccgg tccccaacga tcaaggcgag ttacatgac ccccatgttg tgcaaaaaag | 4705 |
| cggtagctc cttcggtcct ccgatcggtg tcagaagtaa gttggccgca gtgttatcac | 4765 |
| tcatggttat ggcagcactg cataattctc ttactgtcat gccatccgta agatgctttt | 4825 |
| ctgtgactgg tgagtactca accaagtcac tctgagaata gtgtatgcgg cgaccgagtt | 4885 |
| gctcttgccc ggcgtcaata cgggataata ccgcgccaca tagcagaact ttaaaagtgc | 4945 |

2025 RELEASE UNDER E.O. 14176

```
<210> 20
<211> 681
<212> PRT
<213> Artificial Sequence
```

| | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 20 | | | | | | | | | | | | | | | |
| Met | Gly | Lys | Arg | Ser | Ala | Gly | Ser | Ile | Met | Trp | Leu | Ala | Ser | Leu | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Val | Ile | Ala | Gly | Thr | Ser | Ala | Val | Thr | Leu | Val | Arg | Lys | Asn | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Trp | Leu | Leu | Leu | Asn | Val | Thr | Ser | Glu | Asp | Leu | Gly | Lys | Thr | Phe | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Gly | Thr | Gly | Asn | Cys | Thr | Thr | Asn | Ile | Leu | Glu | Ala | Lys | Tyr | Trp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Cys | Pro | Asp | Ser | Met | Glu | Tyr | Asn | Cys | Pro | Asn | Leu | Ser | Pro | Arg | Glu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Glu | Pro | Asp | Asp | Ile | Asp | Cys | Trp | Cys | Tyr | Gly | Val | Glu | Asn | Val | Arg |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Val | Ala | Tyr | Gly | Lys | Cys | Asp | Ser | Ala | Gly | Arg | Ser | Arg | Arg | Ser | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Arg | Ala | Ile | Asp | Leu | Pro | Thr | His | Glu | Asn | His | Gly | Leu | Lys | Thr | Arg |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gln | Glu | Lys | Trp | Met | Thr | Gly | Arg | Met | Gly | Glu | Arg | Gln | Leu | Gln | Lys |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ile | Glu | Arg | Trp | Phe | Val | Arg | Asn | Pro | Phe | Phe | Ala | Val | Thr | Ala | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Thr | Ile | Ala | Tyr | Leu | Val | Gly | Ser | Asn | Met | Thr | Gln | Arg | Val | Val | Ile |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Leu | Leu | Val | Leu | Ala | Val | Gly | Pro | Ala | Tyr | Ser | Ala | His | Cys | Ile |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Gly | Ile | Thr | Asp | Arg | Asp | Phe | Ile | Glu | Gly | Val | His | Gly | Gly | Thr | Trp |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Val | Ser | Ala | Thr | Leu | Glu | Gln | Asp | Lys | Cys | Val | Thr | Val | Met | Ala | Pro |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asp | Lys | Pro | Ser | Leu | Asp | Ile | Ser | Leu | Glu | Thr | Val | Ala | Ile | Asp | Arg |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Pro | Ala | Glu | Val | Arg | Lys | Val | Cys | Tyr | Asn | Ala | Val | Leu | Thr | His | Val |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Lys | Ile | Asn | Asp | Lys | Cys | Pro | Ser | Thr | Gly | Glu | Ala | His | Leu | Ala | Glu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Glu | Asn | Glu | Gly | Asp | Asn | Ala | Cys | Lys | Arg | Thr | Tyr | Ser | Asp | Arg | Gly |
| | | 275 | | | | | 280 | | | | | 285 | | | |

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
 290 295 300
 Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
 305 310 315 320
 Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
 325 330 335
 Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
 340 345 350
 Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
 355 360 365
 Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
 370 375 380
 Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
 385 390 395 400
 Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
 405 410 415
 His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
 420 425 430
 Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
 435 440 445
 Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
 450 455 460
 His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
 465 470 475 480
 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
 485 490 495
 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
 500 505 510
 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
 515 520 525
 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
 530 535 540
 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
 545 550 555 560
 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
 565 570 575
 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
 580 585 590
 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
 595 600 605
 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
 610 615 620
 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
 625 630 635 640
 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
 645 650 655
 Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
 660 665 670
 Met Phe Leu Ser Leu Gly Val Gly Ala
 675 680

<210> 21

<211> 5304

<212> DNA

<220>

<221> CDS

 $\langle 222 \rangle \quad (910) \dots (2986)$

<400> 21

| | | | | | | |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| gacggatcgg | gagatctccc | gatccccctat | ggtcgactct | cagtacaatc | tgtctgatg | 60 |
| ccgcatagtt | aagccagtat | ctgctccctg | cttggtgtgt | ggaggtcgct | gagtagtgcg | 120 |
| cgagcaaaat | ttaagctaca | acaaggcaag | gcttgaccga | caattgcatg | agaatctgc | 180 |
| ttagggttag | gcgttttgcg | ctgcttcgcg | atgtacgggc | cagatatacg | cgttgacatt | 240 |
| gattattgac | tagttattaa | tagtaatcaa | ttacggggtc | attagttcat | agcccatata | 300 |
| tggagttccg | cgttacataa | cttacggtaa | atggcccgcg | tggctgaccg | ccaacgacc | 360 |
| cccgccatt | gacgtcaata | atgacgtatg | ttcccatagt | aacgccata | gggactttcc | 420 |
| attgacgtca | atgggtggac | tatttacggg | aaactgccca | cttggcagta | catcaagtgt | 480 |
| atcatatgcc | aagtacgccc | cctattgacg | tcaatgacgg | taaatggccc | gcctggcatt | 540 |
| atgcccagta | catgacctta | tgggactttc | ctacttgcca | gtacatctac | gtattagtca | 600 |
| tcgctattac | catggtgatg | cggttttggc | agtacatcaa | tgggcgtgga | tagcggtttg | 660 |
| actcacgggg | atttccaagt | ctccacccca | ttgacgtcaa | tgggagtttg | ttttggcacc | 720 |
| aaaatcaacg | ggactttcca | aaatgtcgta | acaactccgc | cccattgacg | caaatgggcg | 780 |
| gtaggcgtgt | acgggtgggag | gtctatataa | gcagagctct | ctggctaact | agagaaccca | 840 |
| ctgcttactg | gcttatcgaa | attaatacga | ctcactatag | ggagacccaa | gcttggtacc | 900 |
| gccgccgcc | atg ggc aag | agg tcc gcc | ggc tca atc | atg tgg ctc | gcg agc | 951 |
| | Met Gly Lys | Arg Ser Ala | Gly Ser Ile | Met Trp | Leu Ala Ser | |
| | 1 | 5 | 10 | | | |

ttg gca gtt gtc ata gct ggt aca agc gct ttg cag tta tca acc tat 999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr
 15 20 25 30

cag ggg aaa gtg tta atg tca atc aac aag act gac gct caa agc gcc 1047
Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala
35 40 45

ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct 1095
Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala
50 55 60

cta gat gtg ggg gtc atg tgc aaa gat gac atc aca tac ctg tgc cca 1143
Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro
65 70 75

gtg ctt tca gcg gga aat gat ccc gag gac att gac tgt tgg tgt gac 1191
Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp
80 85 90

```
gtc gaa gag gtg tgg gtg cac tac ggc aga tgc acg cgc atg gga cat      1239
Val Glu Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His
    95                      100                      105                      110
```

tcg agg cgt agc cga cgg tca atc tct gtg caa cat cat qga gat tcc 1287

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Ser | Arg | Arg | Ser | Arg | Arg | Ser | Ile | Ser | Val | Gln | His | His | Gly | Asp | Ser | |
| | | | | 115 | | | | | 120 | | | | | 125 | | |
| aca | ctg | gca | aca | aag | aac | acg | cca | tgg | ttg | gac | acc | gtg | aaa | acc | acc | 1335 |
| Thr | Leu | Ala | Thr | Lys | Asn | Thr | Pro | Trp | Leu | Asp | Thr | Val | Lys | Thr | Thr | |
| | | | 130 | | | | | 135 | | | | | 140 | | | |
| aaa | tac | ttg | aca | aaa | gta | gaa | aac | tgg | gtt | ttg | cgc | aat | cct | gga | tat | 1383 |
| Lys | Tyr | Leu | Thr | Lys | Val | Glu | Asn | Trp | Val | Leu | Arg | Asn | Pro | Gly | Tyr | |
| | | 145 | | | | | 150 | | | | | 155 | | | | |
| gcc | cta | gtt | gcg | ctg | gcg | att | gga | tgg | atg | ctc | ggt | agc | aac | aac | aca | 1431 |
| Ala | Leu | Val | Ala | Leu | Ala | Ile | Gly | Trp | Met | Leu | Gly | Ser | Asn | Asn | Thr | |
| | 160 | | | | | 165 | | | | | 170 | | | | | |
| cag | aga | gtg | gtt | ttt | gtg | atc | atg | ctg | atg | ctg | att | gct | ccg | gca | tac | 1479 |
| Gln | Arg | Val | Val | Phe | Val | Ile | Met | Leu | Met | Leu | Ile | Ala | Pro | Ala | Tyr | |
| 175 | | | | 180 | | | | | | 185 | | | | | 190 | |
| agc | ttc | aac | tgt | ctg | gga | aca | tca | aac | agg | gac | ttt | gtc | gag | gga | gcc | 1527 |
| Ser | Phe | Asn | Cys | Leu | Gly | Thr | Ser | Asn | Arg | Asp | Phe | Val | Glu | Gly | Ala | |
| | | | 195 | | | | | 200 | | | | | | 205 | | |
| agt | ggg | gca | aca | tgg | att | gac | ttg | gta | ctt | gaa | ggg | gga | agc | tgt | gtc | 1575 |
| Ser | Gly | Ala | Thr | Trp | Ile | Asp | Leu | Val | Leu | Glu | Gly | Gly | Ser | Cys | Val | |
| | | | 210 | | | | 215 | | | | | | 220 | | | |
| aca | gtg | atg | gca | cca | gag | aaa | cca | aca | ctg | gac | ttc | aaa | gtg | atg | aag | 1623 |
| Thr | Val | Met | Ala | Pro | Glu | Lys | Pro | Thr | Leu | Asp | Phe | Lys | Val | Met | Lys | |
| | | 225 | | | | | 230 | | | | | 235 | | | | |
| atg | gag | gct | acc | gag | tta | gcc | act | gtg | cgt | gag | tat | tgt | tac | gaa | gca | 1671 |
| Met | Glu | Ala | Thr | Glu | Leu | Ala | Thr | Val | Arg | Glu | Tyr | Cys | Tyr | Glu | Ala | |
| | 240 | | | | | 245 | | | | | 250 | | | | | |
| acc | ttg | gac | acg | ctg | tca | aca | gtg | gca | agg | tgc | ccc | aca | aca | gga | gaa | 1719 |
| Thr | Leu | Asp | Thr | Leu | Ser | Thr | Val | Ala | Arg | Cys | Pro | Thr | Thr | Gly | Glu | |
| 255 | | | | 260 | | | | | | 265 | | | | | 270 | |
| gct | cac | aac | acc | aaa | agg | agt | gac | cca | aca | ttt | gtc | tgc | aaa | aga | gat | 1767 |
| Ala | His | Asn | Thr | Lys | Arg | Ser | Asp | Pro | Thr | Phe | Val | Cys | Lys | Arg | Asp | |
| | | | 275 | | | | | 280 | | | | | | 285 | | |
| gtt | gtg | gac | cgc | gga | tgg | ggt | aac | gga | tgt | ggt | ctg | ttt | gga | aaa | ggg | 1815 |
| Val | Val | Asp | Arg | Gly | Trp | Gly | Asn | Gly | Cys | Gly | Leu | Phe | Gly | Lys | Gly | |
| | | | 290 | | | | 295 | | | | | | 300 | | | |
| agc | att | gac | aca | tgc | gct | aag | ttc | aca | tgc | aaa | aac | aag | gca | aca | ggg | 1863 |
| Ser | Ile | Asp | Thr | Cys | Ala | Lys | Phe | Thr | Cys | Lys | Asn | Lys | Ala | Thr | Gly | |
| | | 305 | | | | | 310 | | | | | 315 | | | | |
| aag | acg | atc | ttg | aga | gaa | aac | atc | aag | tat | gag | gtt | gca | atc | ttt | gtg | 1911 |
| Lys | Thr | Ile | Leu | Arg | Glu | Asn | Ile | Lys | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| cat | ggt | tca | acg | gac | tct | acg | tca | cat | ggc | aat | tac | tct | gag | cag | att | 1959 |
| His | Gly | Ser | Thr | Asp | Ser | Thr | Ser | His | Gly | Asn | Tyr | Ser | Glu | Gln | Ile | |
| 335 | | | | | 340 | | | | | 345 | | | | | 350 | |
| gga | aaa | aac | caa | gcg | gct | aga | ttc | acc | ata | agc | ccg | caa | gca | ccg | tcc | 2007 |
| Gly | Lys | Asn | Gln | Ala | Ala | Arg | Phe | Thr | Ile | Ser | Pro | Gln | Ala | Pro | Ser | |
| | | | | 355 | | | | | 360 | | | | | 365 | | |
| ttt | acg | gcc | aac | atg | ggc | gag | tat | gga | aca | gtt | acc | att | gat | tgt | gaa | 2055 |
| Phe | Thr | Ala | Asn | Met | Gly | Glu | Tyr | Gly | Thr | Val | Thr | Ile | Asp | Cys | Glu | |
| | | | 370 | | | | | 375 | | | | | 380 | | | |
| gca | aga | tca | gga | atc | aac | acg | gag | gat | tat | tat | gtt | ttc | act | gtc | aag | 2103 |
| Ala | Arg | Ser | Gly | Ile | Asn | Thr | Glu | Asp | Tyr | Tyr | Val | Phe | Thr | Val | Lys | |
| | | 385 | | | | | 390 | | | | | 395 | | | | |
| gag | aag | tca | tgg | cta | gtg | aac | agg | gac | tgg | ttt | cac | gac | ttg | aac | ctt | 2151 |
| Glu | Lys | Ser | Trp | Leu | Val | Asn | Arg | Asp | Trp | Phe | His | Asp | Leu | Asn | Leu | |
| | 400 | | | | | 405 | | | | | 410 | | | | | |
| cca | tgg | acg | agc | cct | gcc | aca | act | gat | tgg | cgc | aac | aga | gaa | aca | ctg | 2199 |
| Pro | Trp | Thr | Ser | Pro | Ala | Thr | Thr | Asp | Trp | Arg | Asn | Arg | Glu | Thr | Leu | |
| 415 | | | | | 420 | | | | | 425 | | | | | 430 | |
| gtg | gaa | ttt | gag | gaa | ccg | cat | gcc | acc | aag | caa | act | gta | gta | gcc | cta | 2247 |
| Val | Glu | Phe | Glu | Glu | Pro | His | Ala | Thr | Lys | Gln | Thr | Val | Val | Ala | Leu | |
| | | | | 435 | | | | | 440 | | | | | 445 | | |
| gga | tcg | caa | gaa | ggt | gcc | ctg | cac | aca | gca | ttg | gct | gga | gcc | att | cca | 2295 |
| Gly | Ser | Gln | Glu | Gly | Ala | Leu | His | Thr | Ala | Leu | Ala | Gly | Ala | Ile | Pro | |
| | | | 450 | | | | | 455 | | | | | 460 | | | |
| gcc | act | gtt | agc | agc | tca | acc | cta | acc | ttg | caa | tca | ggg | cat | ttg | aaa | 2343 |
| Ala | Thr | Val | Ser | Ser | Ser | Thr | Leu | Thr | Leu | Gln | Ser | Gly | His | Leu | Lys | |
| | | 465 | | | | | 470 | | | | | 475 | | | | |
| tgc | aga | gct | aag | ctt | gac | aag | gtc | aaa | atc | aag | gga | acg | aca | tat | ggc | 2391 |
| Cys | Arg | Ala | Lys | Leu | Asp | Lys | Val | Lys | Ile | Lys | Gly | Thr | Thr | Tyr | Gly | |
| | 480 | | | | | 485 | | | | | 490 | | | | | |
| atg | tgt | gac | tct | gcc | ttc | acc | ttc | agc | aag | aac | cca | act | gac | aca | ggg | 2439 |
| Met | Cys | Asp | Ser | Ala | Phe | Thr | Phe | Ser | Lys | Asn | Pro | Thr | Asp | Thr | Gly | |
| 495 | | | | | 500 | | | | | 505 | | | | | 510 | |
| cac | ggg | aca | gtg | att | gtg | gaa | ctg | cag | tat | act | gga | agc | aac | gga | ccc | 2487 |
| His | Gly | Thr | Val | Ile | Val | Glu | Leu | Gln | Tyr | Thr | Gly | Ser | Asn | Gly | Pro | |
| | | | | 515 | | | | | 520 | | | | | 525 | | |
| tgc | cga | gtt | ccc | atc | tcc | gtg | act | gca | aac | ctc | atg | gat | ttg | aca | ccg | 2535 |
| Cys | Arg | Val | Pro | Ile | Ser | Val | Thr | Ala | Asn | Leu | Met | Asp | Leu | Thr | Pro | |
| | | | 530 | | | | | 535 | | | | | 540 | | | |
| gtt | gga | aga | ttg | gtc | acg | gtc | aat | ccc | ttt | ata | | | | | | |

| | |
|---|------|
| Val Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala | |
| 545 550 555 | |
| aac aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac | 2631 |
| Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr | |
| 560 565 570 | |
| atc gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa | 2679 |
| Ile Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys | |
| 575 580 585 590 | |
| gag gga agc agc att ggg aag gct ttg gcg acc aca tgg aaa gga gcc | 2727 |
| Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala | |
| 595 600 605 | |
| caa cgg cta gcc gtc tta ggg gac aca gcg tgg gac ttt gga tct att | 2775 |
| Gln Arg Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile | |
| 610 615 620 | |
| gga gga gtt ttc aat tca att ggc aaa gct gtc cac caa gtt ttc gga | 2823 |
| Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly | |
| 625 630 635 | |
| gga gcg ttc agg act ctg ttc ggg gga atg tcc tgg atc aca cag ggg | 2871 |
| Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly | |
| 640 645 650 | |
| cta ctt gga gct ctt ctc ctg tgg atg ggg ttg cag gcc cgc gac agg | 2919 |
| Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg | |
| 655 660 665 670 | |
| agc atc tcg ctg act cta ctg gct gtc gga ggg att ctc atc ttt ctg | 2967 |
| Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu | |
| 675 680 685 | |
| gca acc agc gtg caa gcc t gagcgccgc tcgagcatgc atctagaggg | 3016 |
| Ala Thr Ser Val Gln Ala | |
| 690 | |
| ccctattcta tagtgtcacc taaatgctag agctcgctga tcagcctcga ctgtgccttc | 3076 |
| tagttgccag ccattctgttg tttgccccctc ccccggtgect tccttgaccc tggaagggtgc | 3136 |
| cactcccact gtccttttcc aataaaatga ggaaattgca tcgcattgtc tgagtaggtg | 3196 |
| tcattctatt ctgggggggtg ggggtggggca ggacagcaag ggggaggatt gggaagacaa | 3256 |
| tagcaggcat gctgggggatg cgggtgggctc tatggcttct gaggcggaaa gaacagctgc | 3316 |
| attaatgaat cggccaacgc gcggggagag gcgggtttgcg tattgggcgc tcttccgctt | 3376 |
| cctcgctcac tgactcgctg cgctcggtcg ttccgctgcg gcgagcggta tcagctcact | 3436 |
| caaaggcggg aatacgggta tccacagaat caggggataa cgcaggaaag aacatgtgag | 3496 |
| caaaaggcca gcaaaaggcc aggaaccgta aaaaggccgc gttgctggcg tttttccata | 3556 |
| ggctccgccc ccctgacgag catcacaaaa atcgacgctc aagtacagagg tggcgaaacc | 3616 |
| cgacaggact ataaagatac caggcggtttc cccctggaag ctccctcgctg cgctctcctg | 3676 |
| ttccgacctt gccgcttacc ggatacctgt ccgcctttct cccttcggga agcgtggcgc | 3736 |
| tttctcaatg ctcacgctgt aggtatctca gttcggtgta ggtcgttcgc tccaagctgg | 3796 |
| gctgtgtgca cgaaccccc gttcagcccc accgctgcgc cttatccggt aactatcgctc | 3856 |
| ttgagtccaa cccggtaaga cagcacttat cgccactggc agcagccact ggtaacagga | 3916 |

2025-07-23 14:11:40

```

ttagcagagc gaggtatgta ggcggtgcta cagagttctt gaagtgggtgg cctaactacg 3976
gctacactag aaggacagta tttggtatct gcgctctgct gaagccagtt accttcggaa 4036
aaagagttgg tagctcttga tccggcaaac aaaccaccgc tggtagcggg ggtttttttg 4096
tttgcaagca gcagattacg cgcagaaaaa aaggatctca agaagatcct ttgatctttt 4156
ctacgggggc tgacgctcag tggaaacgaaa actcacgtta agggattttg gtcatgagat 4216
tatcaaaaag gatcttcacc tagatccttt taaattaaaa atgaagtttt aaatcaatct 4276
aaagtatata tgagtaaact tgggtctgaca gttaccaatg cttaatcagt gaggcaccta 4336
tctcagcgat ctgtctatct cgttcatcca tagttgcctg actccccgctc gtgtagataa 4396
ctacgatacg ggagggctta ccatctggcc ccagtgtctg aatgataccg cgagaccac 4456
gctcaccggc tccagattta tcagcaataa accagccagc cggaaggggc gagcgcagaa 4516
gtggctctgc aactttatcc gctccatcc agtctattaa ttgttgccgg gaagctagag 4576
taagtagttc gccagttaat agtttgcgca acgttggtgc cattgctaca ggcacgtgg 4636
tgtcacgctc gtcgtttggg atggcttcat tcagctccgg ttccaacga tcaaggcgag 4696
ttacatgatc ccccatggtg tgcaaaaaag cggttagctc cttcggtcct ccgatcggtg 4756
tcagaagtaa gttggccgca gtgttatcac tcatgggtat ggcagcactg cataattctc 4816
ttactgtcat gccatccgta agatgctttt ctgtgactgg tgagtactca accaagtcac 4876
tctgagaata gtgtatgcgg cgaccgagtt gctcttgccc ggcgtcaata cgggataata 4936
ccgcgccaca tagcagaact ttaaaagtgc tcatcattgg aaaacgttct tcggggcgaa 4996
aactctcaag gatcttaccg ctgttgagat ccagttcgat gtaaccact cgtgcacca 5056
actgatcttc agcatctttt actttcacca gcgtttctgg gtgagcaaaa acaggaaggc 5116
aaaatgccgc aaaaaaggga ataaggcgca cacggaaatg ttgaatactc atactcttcc 5176
tttttcaata ttattgaagc atttatcagg gttattgtct catgagcgga tacatatttg 5236
aatgtattta gaaaaataaa caaatagggg ttccgcgcac atttccccga aaagtgccac 5296
ctgacgtc 5304

```

<210> 22

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 22

```

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1           5           10           15
Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly
20           25           30
Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
35           40           45
Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
50           55           60
Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
65           70           75           80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
85           90           95
Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
100          105          110
Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
115          120          125
Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
130          135          140

```

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu
 145 150 155 160
 Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
 165 170 175
 Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
 180 185 190
 Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
 195 200 205
 Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val
 210 215 220
 Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu
 225 230 235 240
 Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu
 245 250 255
 Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His
 260 265 270
 Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val
 275 280 285
 Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
 290 295 300
 Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr
 305 310 315 320
 Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
 325 330 335
 Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys
 340 345 350
 Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr
 355 360 365
 Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg
 370 375 380
 Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys
 385 390 395 400
 Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp
 405 410 415
 Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu
 420 425 430
 Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser
 435 440 445
 Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr
 450 455 460
 Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg
 465 470 475 480
 Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys
 485 490 495
 Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly
 500 505 510
 Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg
 515 520 525
 Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly
 530 535 540
 Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn
 545 550 555 560
 Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
 565 570 575

14114.0332U3
 ATTORNEY DOCKET NO.

Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly
 580 585 590
 Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg
 595 600 605
 Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
 610 615 620
 Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
 625 630 635 640
 Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
 645 650 655
 Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile
 660 665 670
 Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr
 675 680 685
 Ser Val Gln Ala
 690

<210> 23

<211> 5271

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<221> CDS

<222> (910)...(2953)

<400> 23

gacggatcgg gagatctccc gatccccctat ggtcgactct cagtacaatc tgctctgatg 60
 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
 ttagggttag gcggttttgcg ctgcttcgog atgtacgggc cagatatacg cgttgacatt 240
 gattattgac tagttatttaa tagtaatcaa ttacgggggc attagtcat agcccatata 300
 tggagttccg cgttacataa cttacggtaa atggcccggc tggctgaccg cccaacgacc 360
 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
 attgacgtca atgggtggac tatttaagggt aaactgccc cttggcagta catcaagtgt 480
 atcatatgcc aagtagcccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
 atgcccagta catgacctta tgggaacttc ctacttggca gtacatctac gtattagtca 600
 tcgctattac catggtgatg cgggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780
 gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccga 840
 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc 900
 gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
 1 5 10

ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa 999
 Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys
 15 20 25 30

aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca 1047

ATTORNEY DOCKET NO. 14114.0332U3

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Asn | Arg | Trp | Leu | Leu | Leu | Asn | Val | Thr | Ser | Glu | Asp | Leu | Gly | Lys | Thr | | |
| | | | | 35 | | | | | 40 | | | | | 45 | | | |
| ttc | tct | gtg | ggc | aca | ggc | aac | tgc | aca | aca | aac | att | ttg | gaa | gcc | aag | 1095 | |
| Phe | Ser | Val | Gly | Thr | Gly | Asn | Cys | Thr | Thr | Asn | Ile | Leu | Glu | Ala | Lys | | |
| | | | 50 | | | | | 55 | | | | | 60 | | | | |
| tac | tgg | tgc | cca | gac | tca | atg | gaa | tac | aac | tgt | ccc | aat | ctc | agt | cca | 1143 | |
| Tyr | Trp | Cys | Pro | Asp | Ser | Met | Glu | Tyr | Asn | Cys | Pro | Asn | Leu | Ser | Pro | | |
| | | 65 | | | | | 70 | | | | | 75 | | | | | |
| aga | gag | gag | cca | gat | gac | att | gat | tgc | tgg | tgc | tat | ggg | gtg | gaa | aac | 1191 | |
| Arg | Glu | Glu | Pro | Asp | Asp | Ile | Asp | Cys | Trp | Cys | Tyr | Gly | Val | Glu | Asn | | |
| | 80 | | | | | 85 | | | | | 90 | | | | | | |
| gtt | aga | gtc | gca | tat | ggt | aag | tgt | gac | tca | gca | ggc | agg | tct | agg | agg | 1239 | |
| Val | Arg | Val | Ala | Tyr | Gly | Lys | Cys | Asp | Ser | Ala | Gly | Arg | Ser | Arg | Arg | | |
| | 95 | | | | 100 | | | | | 105 | | | | | 110 | | |
| tca | aga | agg | gcc | att | gac | ttg | cct | acg | cat | gaa | aac | cat | ggt | ttg | aag | 1287 | |
| Ser | Arg | Arg | Ala | Ile | Asp | Leu | Pro | Thr | His | Glu | Asn | His | Gly | Leu | Lys | | |
| | | | | 115 | | | | | 120 | | | | | 125 | | | |
| acc | cgg | caa | gaa | aaa | tgg | atg | act | gga | aga | atg | ggt | gaa | agg | caa | ctc | 1335 | |
| Thr | Arg | Gln | Glu | Lys | Trp | Met | Thr | Gly | Arg | Met | Gly | Glu | Arg | Gln | Leu | | |
| | | 130 | | | | | | 135 | | | | | 140 | | | | |
| caa | aag | att | gag | aga | tgg | ttc | gtg | agg | aac | ccc | ttt | ttt | gca | gtg | acg | 1383 | |
| Gln | Lys | Ile | Glu | Arg | Trp | Phe | Val | Arg | Asn | Pro | Phe | Phe | Ala | Val | Thr | | |
| | 145 | | | | | | 150 | | | | | 155 | | | | | |
| gct | ctg | acc | att | gcc | tac | ctt | gtg | gga | agc | aac | atg | acg | caa | cga | gtc | 1431 | |
| Ala | Leu | Thr | Ile | Ala | Tyr | Leu | Val | Gly | Ser | Asn | Met | Thr | Gln | Arg | Val | | |
| | 160 | | | | | 165 | | | | | 170 | | | | | | |
| gtg | att | gcc | cta | ctg | gtc | ttg | gct | gtt | ggt | ccg | gcc | tac | tca | gct | cac | 1479 | |
| Val | Ile | Ala | Leu | Leu | Val | Leu | Ala | Val | Gly | Pro | Ala | Tyr | Ser | Ala | His | | |
| | 175 | | | | 180 | | | | | 185 | | | | | 190 | | |
| tgc | att | gga | att | act | gac | agg | gat | ttc | att | gag | ggg | gtg | cat | gga | gga | 1527 | |
| Cys | Ile | Gly | Ile | Thr | Asp | Arg | Asp | Phe | Ile | Glu | Gly | Val | His | Gly | Gly | | |
| | | | | 195 | | | | | 200 | | | | | 205 | | | |
| act | tgg | gtt | tca | gct | acc | ctg | gag | caa | gac | aag | tgt | gtc | act | gtt | atg | 1575 | |
| Thr | Trp | Val | Ser | Ala | Thr | Leu | Glu | Gln | Asp | Lys | Cys | Val | Thr | Val | Met | | |
| | | 210 | | | | | | 215 | | | | | 220 | | | | |
| gcc | cct | gac | aag | cct | tca | ttg | gac | atc | tca | cta | gag | aca | gta | gcc | att | 1623 | |
| Ala | Pro | Asp | Lys | Pro | Ser | Leu | Asp | Ile | Ser | Leu | Glu | Thr | Val | Ala | Ile | | |
| | | 225 | | | | | 230 | | | | | 235 | | | | | |
| gat | aga | cct | gct | gag | gtg | agg | aaa | gtg | tgt | tac | aat | gca | gtt | ctc | act | 1671 | |
| Asp | Arg | Pro | Ala | Glu | Val | Arg | Lys | Val | Cys | Tyr | Asn | Ala | Val | Leu | Thr | | |
| | 240 | | | | | 245 | | | | | 250 | | | | | | |

T04060360

| | |
|---|------|
| cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta | 1719 |
| His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu | |
| 255 260 265 270 | |
| gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat | 1767 |
| Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp | |
| 275 280 285 | |
| aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg | 1815 |
| Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val | |
| 290 295 300 | |
| gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt | 1863 |
| Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val | |
| 305 310 315 | |
| gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg | 1911 |
| Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly | |
| 320 325 330 | |
| gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat | 1959 |
| Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp | |
| 335 340 345 350 | |
| gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct | 2007 |
| Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala | |
| 355 360 365 | |
| aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac | 2055 |
| Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr | |
| 370 375 380 | |
| atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc | 2103 |
| Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala | |
| 385 390 395 | |
| cag gac ttg acc ctg cca tgg cag agt gga agt ggc ggg gtg tgg aga | 2151 |
| Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg | |
| 400 405 410 | |
| gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc | 2199 |
| Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile | |
| 415 420 425 430 | |
| aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt | 2247 |
| Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu | |
| 435 440 445 | |
| act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac | 2295 |
| Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr | |
| 450 455 460 | |
| aaa cta cat ggt gga cat gtt tct tgc aga gtg aaa ttg tca gct ttg | 2343 |

T04040-573360

| | |
|---|-------------|
| Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu | |
| 465 | 470 475 |
| aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt | 2391 |
| Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe | |
| 480 | 485 490 |
| gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg | 2439 |
| Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val | |
| 495 | 500 505 510 |
| aaa gtg tca aaa gga gcc ccc tgc agg att cca gtg ata gta gct gat | 2487 |
| Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp | |
| | 515 520 525 |
| gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc | 2535 |
| Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro | |
| | 530 535 540 |
| atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct | 2583 |
| Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro | |
| | 545 550 555 |
| ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act | 2631 |
| Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr | |
| | 560 565 570 |
| tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag | 2679 |
| Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln | |
| 575 | 580 585 590 |
| acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg | 2727 |
| Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp | |
| | 595 600 605 |
| gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att | 2775 |
| Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile | |
| | 610 615 620 |
| cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac | 2823 |
| His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn | |
| | 625 630 635 |
| tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc | 2871 |
| Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile | |
| | 640 645 650 |
| aac aca aga aac atg aca atg tcc atg agc atg atc ttg gta gga gtg | 2919 |
| Asn Thr Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val | |
| 655 | 660 665 670 |
| atc atg atg ttt ttg tct cta gga gtt ggg gcg t gagcggccgc | 2963 |
| Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala | |
| | 675 680 |

2025 RELEASED

tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaatgctag agctcgctga 3023
tcagcctcga ctgtgccttc tagttgccag ccatctgttg tttgcccctc ccccgctgct 3083
tccttgaccc tgggaagggtgc cactcccact gtccttttct aataaaatga ggaaattgca 3143
tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag 3203
ggggaggatt gggaagacaa tagcaggcat gctggggatg cgggtgggctc tatggcttct 3263
gaggcgga aaacagctgc attaatgaat cgcccaacgc gcggggagag gcggtttgctg 3323
tattgggcgc tcttcgcctt cctcgctcac tgactcgctg cgctcggtcg ttcggctgctg 3383
gcgagcggta tcagctcact caaaggcggg aatacgggta tccacagaat caggggataa 3443
cgcaggaaag aacatgtgag caaaaggcca gcaaaaggcc aggaaccgta aaaaggccgc 3503
gttgctggcg tttttccata ggctccgccc cctgacgag catcacaaaa atcgacgctc 3563
aagtcagagg tggcgaaacc cgacaggact ataaagatac caggcgtttc cccctggaag 3623
ctccctcgctg cgctctcctg ttccgacctt gccgcttacc ggatacctgt ccgcctttct 3683
cccttcggga agcgtggcgc tttctcaatg ctacgctgt aggtatctca gttcggtgta 3743
ggctgcttgc tccaagctgg gctgtgtgca cgaacccccc gttcagcccg accgctgctg 3803
cttatccggg aactatcgct ttgagtccaa cccggtaaga cagcacttat cgccactggc 3863
agcagccact ggtaacagga ttagcagagc gaggtatgta ggcggtgcta cagagttctt 3923
gaagtgggtg cctaactacg gctacactag aaggacagta tttggtatct gcgctctgct 3983
gaagccagtt accttcggaa aaagagttgg tagctcttga tccggcaaac aaaccaccgc 4043
tggtagcggg ggtttttttg tttgcaagca gcagattacg cgcagaaaaa aaggatctca 4103
agaagatcct ttgatctttt ctacgggggtc tgacgctcag tggaacgaaa actcacgtta 4163
agggattttg gtcattgagat tatcaaaaag gatcttcacc tagatccttt taaattaaaa 4223
atgaagtttt aaatcaatct aaagtatata tgagtaaact tggctctgaca gttaccaatg 4283
cttaatcagt gaggcaccta tctcagcgat ctgtctatct cgttcatcca tagttgcctg 4343
actccccgtc gtgtagataa ctacgatacg ggagggctta ccatctggcc ccagtgtgct 4403
aatgataccg cgagacccac gctcaccggc tccagattta tcagcaataa accagccagc 4463
cggaaggggc gagcgcagaa gtgggtcctgc aactttatcc gcctccatcc agtctattaa 4523
ttgttgccgg gaagctagag taagtagtto gccagttaat agtttgcgca acgttggtg 4583
cattgctaca ggcatcggtg tgtcacgctc gtcgttttgt atggcttcat tcagctccgg 4643
ttcccaacga tcaaggcgag ttacatgata ccccatgttg tgcaaaaaag cggtttagctc 4703
cttcggtcct ccatcggttg tcagaagtaa gttggccgca gtgttatcac tcatggttat 4763
ggcagcactg cataattctc ttactgtcat gccatccgta agatgctttt ctgtgactgg 4823
tgagtactca accaagtcac tctgagaata gtgtatgcgg cgaccgagtt gctcttgccc 4883
ggcgtcaata cgggataata ccgcgccaca tagcagaact ttaaaagtgc tcatcattgg 4943
aaaacgttct tcggggcgaa aactctcaag gatcttaccg ctgttgagat ccagttcgat 5003
gtaacccact cgtgcaccca actgatcttc agcatctttt actttcacca gcgtttctg 5063
gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga ataaggcgca cacggaaatg 5123
ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg gttattgtct 5183
catgagcggg tacatatattg aatgtattta gaaaaataaa caaatagggg ttccgcgcac 5243
atttccccga aaagtgccac ctgacgctc 5271

<210> 24

<211> 681

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 24

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala

1

5

10

15

[illegible]

Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
 450 455 460
 His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
 465 470 475 480
 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
 485 490 495
 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
 500 505 510
 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
 515 520 525
 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
 530 535 540
 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
 545 550 555 560
 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
 565 570 575
 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
 580 585 590
 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
 595 600 605
 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
 610 615 620
 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
 625 630 635 640
 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
 645 650 655
 Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
 660 665 670
 Met Phe Leu Ser Leu Gly Val Gly Ala
 675 680

<210> 25
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> misc_feature
 <222> 1-35
 <223> POW 454

<400> 25
 aaaagaaaaa gcgctaccac catccaccgg gacag

35

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

ATTORNEY DOCKET NO. 14114.0332U3

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-41

<223> CPOW 2417

<400> 26

actggttacc tcaaccccggt actcgccggc gaaaaagaaa a

41

<210> 27

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> Modified JE Signal

<400> 27

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala

1

5

10

15

Val Val Ile Ala Gly Thr Ser Ala

20

<210> 28

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-36

<223> YF 482

<400> 28

aaaagaaaaa ggcgtgtgac cttggtgcgg aaaaaa

36

<210> 29

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

SEQUENCE LISTING

<221> misc_feature
<222> 1-41
<223> CYF 2433

<400> 29
acagagatcc tcaaccccg c actcgccggc gaaaaagaaa a

41

<210> 30
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-41
<223> SLE 463

<400> 30
aaaagaaaaa gcgctttgca gttatcaacc tatcagggga a

41

<210> 31
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-40
<223> CSLE 2477

<400> 31
accgttggtc gcacgttcgg actcgccggc gaaaaagaaa

40

ATTORNEY DOCKET NO. 14114.0332U3